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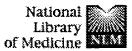
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	L29	L28 AND tyrosine kinase	128
	L28	L27 AND insulin receptor	164
	L27	PIR	23861
	L26	hGrb14	0
	L25	L24 AND insulin receptor	45
	L24	L22 AND PIR	523
	L23	L22 AND hGrb14	0
	L22	530/300,324,350.CCLS.	18881
	L21	L20 AND insulin receptor	23
	L20	L18 AND PIR	165
	L19	L18 AND hGrb14	0
	L18	435/7.1,7.2.CCLS.	10015
	L17	Girard-J.IN.	115
	L16	Girard-Jean.IN.	5
	L15	Girard.IN.	2870
	L14	Bereziat-V.IN.	1
	L13	Bereziat-Veronique.IN.	1
	L12	Bereziat.IN.	36
	L11	Kasus-Jacobi-Anne.IN.	1
	L10	Kasus-Jacobi-A.IN.	1
	L9	Kasus-Jacobi.IN.	2
	L8	Perdereau-D.IN.	1
	L7	Perdereau-Dominique.IN.	1
	L6	Perdereau.IN.	3
	L5	Burnol-A.IN.	1
	L4	Burnol-A-F.IN.	1
	L3	Burnol-Anne.IN.	0
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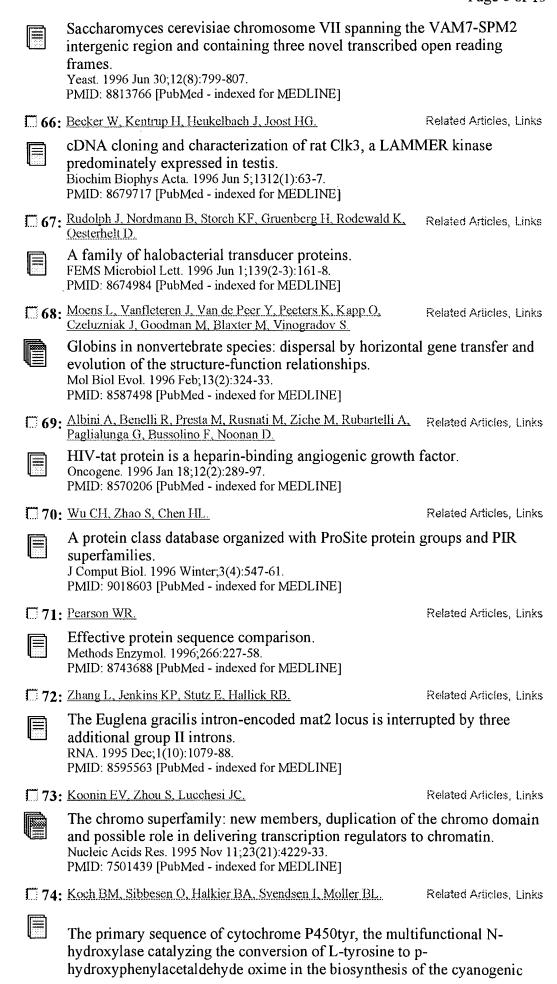
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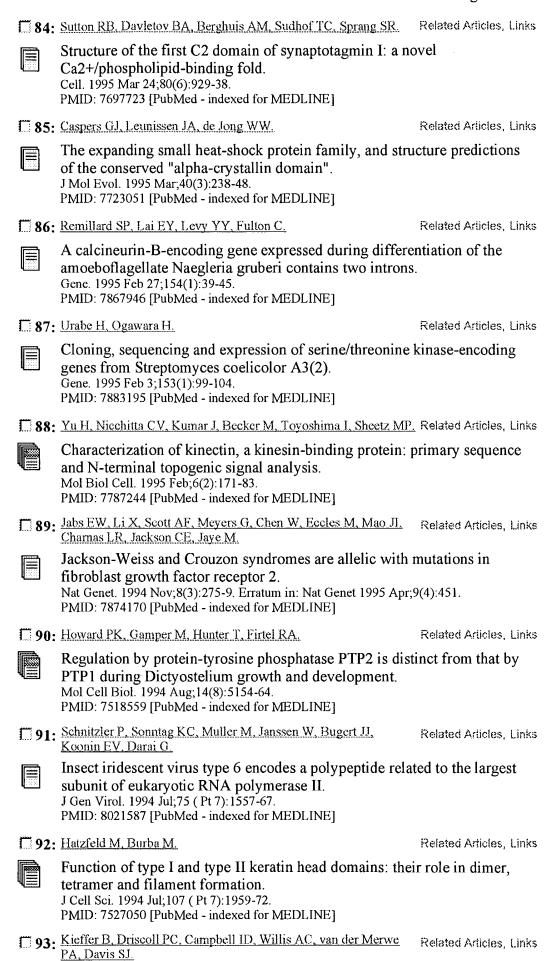
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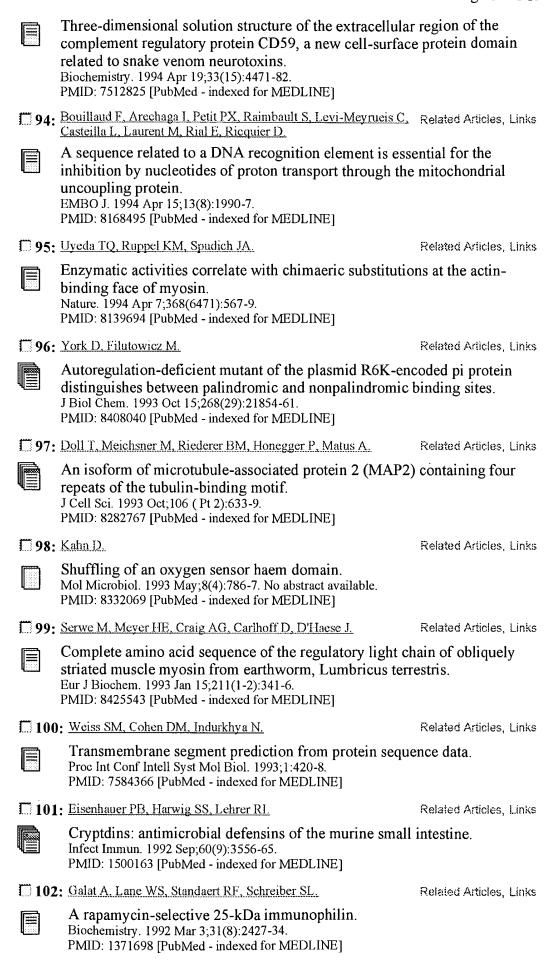
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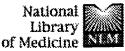
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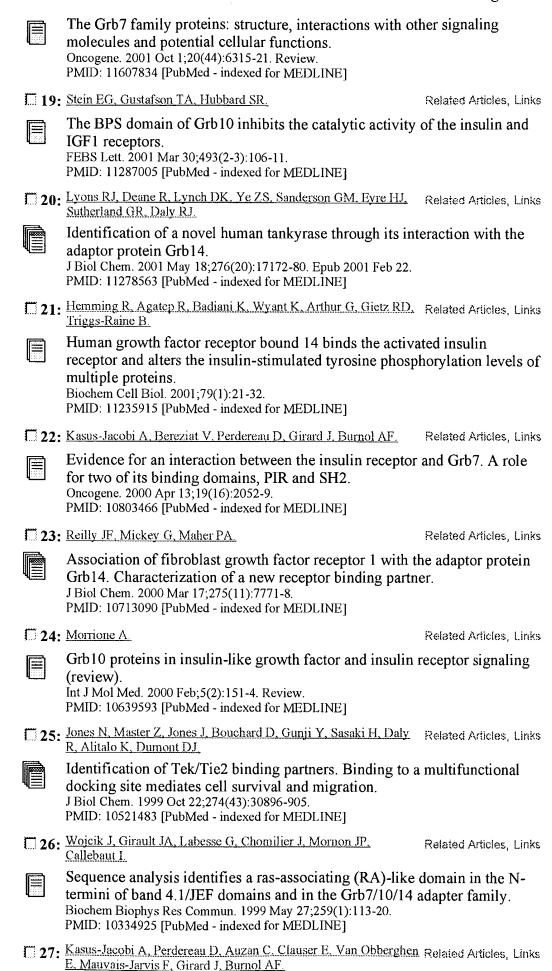
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PROCESSING COMPLETED FOR L1
             156 DUP REM L1 (204 DUPLICATES REMOVED)
=> D L2 1-156
L2
      ANSWER 1 OF 156 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI ON STN
      DUPLICATE 1
      2004-13578
                  BIOTECHDS
AN
      Diagnosing pancreatic cancer (PNC) comprises determining a level of
TT
      expression of a PNC-associated gene in a patient derived biological
          gene expression level determination and antisense sequence for use in
          disease therapy and gene therapy
      NAKAMURA Y; KATAGIRI T
ΑU
      ONCOTHERAPY SCI INC; UNIV TOKYO
PΑ
      WO 2004031412 15 Apr 2004
WO 2003-JP11817 17 Sep 2003
PT
AΤ
      US 2003-450889 28 Feb 2003; US 2002-414872 30 Sep 2002
PRAI
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      English
LA
os
      WPI: 2004-330205 [30]
     ANSWER 2 OF 156 CAPLUS COPYRIGHT 2004 ACS ON STN DUPLICATE 2
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     2004:371064 CAPLUS
AN
     140:373461
DN
     Evaluation of breast cancer states and outcomes using gene expression
TI
     profiles
     West, Mike; Nevins, Joseph R.; Huang, Andrew
IN
PA
     Synpac, Inc., USA
     PCT Int. Appl., 799 pp.
S<sub>0</sub>
     CODEN: PIXXD2
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              PL, PT,
              TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ,
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                               20021112
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     WO 2002-US38216
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     WO 2002-US38222
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AN
     2004:311060
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     140:333607
     Differentially nucleic acids and encoded proteins useful for diagnosing
ΤI
     testicular seminomas
IN
     Nakamura, Yusuke; Katagiri, Toyomasa
     Oncotherapy Science, Inc., Japan; Japan as Represented by the President of
PA
     the University of Tokyo
SO
     PCT Int. Appl., 120 pp.
     CODEN: PIXXD2
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PRAI US 2002-414677P
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      10614099 IFIPAT; IFIUDB; IFICDB
ΑN
      MRNA BINDING MOTIF
TI
      Balmer Lois (AU); Leedman Peter J (AU); Thomson Andrew (AU)
IN
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PA
                       A1 20040624
      US 2004121323
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      US 2000-168781
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      wo 2000-AU1595
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                                       PCT 371 date
                            20001222
                                       PCT 102(e) date
      AU 1999-4835
                            19991223
PRAI
      US 2004121323
                            20040624
FI
      Utility; Patent Application - First Publication
DT
FS
      CHEMICAL
      APPLICATION
CLMN
      14
GΙ
       16 Figure(s).
     FIG. 1 shows a schematic of the Grb7 family members.
     FIG. 2A, FIG. 2B, FIG. 2C, FIG. 2D, FIG. 2E and FIG. 2F show regulation of
      EGF-R mRNA expression by EGF in MDA-468 and BT-20 human breast cancer
      cells, including Northern, Western blot and actinomycin D chase assays.
     FIG. 3A, FIG. 3B, FIG. 3C, FIG. 3D, FIG. 3E, FIG. 3F, FIG. 3G and FIG. 3H
      show a schematic of EGF-R mRNA, the clones generated for transfection and
      RNA electrophoretic gel mobility shift assay (REMSA), as well as data
      from transfections and cell free mRNA decay assay.
     FIG. 4A, FIG. 4B, FIG. 4C, FIG. 4D and FIG. 4E show results of multiple transfections into breast cancer cells, and assays of mRNA decay using
      the LightCycler.
     FIG. 5A and FIG. 5B show REMSA and UV cross-linking assays with a variety
      of cell extracts and riboprobes.
     FIG. 6A and FIG. 6B show specificty of binding for the EGF-R mRNA probe
      used as bait in the yeast three-hybrid screening.
     FIG. 7A, FIG. 7B, FIG. 7C and FIG. 7D show REMSA using sense and antisense
      DNA oligomers, as well as RNA probe mutants to define the RNA binding
      site within the EGF-R bait.
     FIG. 8A, FIG. 8B and FIG. 8C show a schematic of the yeast threehybrid
      screening method, REMSA with Grb7 and other antibodies as well as a UV
      cross-linking Western assay using Grb7 antibodies (SenGupta et al.,
      1996).
     FIG. 9A shows a schematic illustrating the amino acid homology between the
      Grb7 family members and the KH-motif. FIG. 9B and FIG. 9C show the
      predicted secondary structure of the Grb7 mRNA binding motif.
     FIG. 10A and FIG. 10B show a schematic of Grb7 family member GSTfusion
      proteins, a REMSA using GST-Grb7 fusion protein with EGFR mRNA and REMSA
      with unlabeled RNA competitors.
     FIG. 11A, FIG. 11B, FIG. 11C, FIG. 11D, FIG. 11E and FIG. 11F show a schematic of the GST-Grb7 mutants, REMSA using the Grb7 mutants with
      EGF-R 2/2A riboprobe and REMSA with different EGFR mRNA probes with each
      of the mutants demonstrating RNA specificity.
     FIG. 12A and FIG. 12B show the sequence of the erbB-2 riboprobe used, and
      a REMSA showing binding of Grb7 and Grb10 to erbB-1 and erbB-2 mRNA.
     FIG. 13A and FIG. 13B show REMSA binding of Grb7 and two mutants to EGF-R
      and erbB-2 mRNAs, together with sequence comparisons and stem-loop plots
      of the RNA structures.
     FIG. 14A and FIG. 14B show binding by GST-Grb10 and GST- ***Grb14***
      erbB-2 mRNA. A competition REMSA with tRNA using Grb7-M3 mutant confirmed
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specificity to the erbB-2 mRNA probe.

DT

Patent

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EGF-R primers and a western blot of EGF-R levels in cells overexpressing
      Grb7.
     FIG. 16 shows an actinomycin D chase to determine the rate of EGF-R mRNA
      decay in stably transfected MDA-468 cells that overexpress Grb7.
L2
     ANSWER 5 OF 156 CAPLUS COPYRIGHT 2004 ACS on STN
AN
     2004:449883 CAPLUS
     140:402911
DN
     Binary prediction tree modeling with many predictors and its uses in
TI
     clinical and genomic applications
ΙN
     Nevins, Joseph R.; West, Mike; Huang, Andrew T.
PA
     Duke University, USA
SO
     PCT Int. Appl., 886 pp.
     CODEN: PIXXD2
DT
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     English
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        2003-458373P
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     wo 2003-us33946
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L2
     ANSWER 6 OF 156 USPATFULL ON STN
AN
       2004:50778 USPATFULL
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       Gene expression in bladder tumors
ΙN
       Orntoft, Torben F., Aabyhoj, DENMARK
PΙ
                             Α1
       US 2004038207
                                   20040226
AΙ
       US 2001-951968
                                   20010914 (9)
                             Α1
       Division of Ser. No. US 2000-510643, filed on 22 Feb 2000, UNKNOWN
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LN.CNT 28561
       INCLM: 435/006.000
INCL
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IC
        [7]
       ICM: C12Q001-68
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
     ANSWER 7 OF 156 USPATFULL ON STN
L2
AN
       2004:24686 USPATFULL
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FIG. 15A and FIG. 15B show immunoprecipitation reverse transcriptase polymerase chain reaction (IP-RT-PCR) assay using Grb7 antibodies and

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TI
        Methods and compositions for the prediction, diagnosis, prognosis,
        prevention and treatment of malignant neoplasma
        Wirtz, Ralph, Koln, GERMANY, FEDERAL REPUBLIC OF
IN
       Munnes, Marc, Erkráth, GERMÁNY, FEDERAL REPUBLIC OF
Kallabis, Harald, Koln, GERMANY, FEDERAL REPUBLIC OF
        Bayer Aktiengesellschaft, Leverkusen, GERMANY, FEDERAL REPUBLIC OF, D
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        2004:13596 USPATFULL
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        Novel proteins and nucleic acids encoding same
        Guo, Xiaojia, Branford, CT, UNITED STATES
IN
       Fernandes, Elma, Branford, CT, UNITED STATES
Li, Li, Branford, CT, UNITED STATES
Kekuda, Ramesh, Stamford, CT, UNITED STATES
        Liu, Yi, New Haven, CT, UNITED STATES
        Leite, Mario, Milford, CT, UNITED STATES
        Spytek, Kimberly A., New Haven, CT, UNITED STATES
        Ji, Weizhen, Branford, CT, UNITED STATES
        Casman, Stacie J., North Haven, CT, UNITED STATES
        Boldog, Ference L., North Haven, CT, UNITED STATES
        Patturajan, Meera, Branford, CT, UNITED STATES
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        Ballinger, Robert A., Newington, CT, UNITED STATES Malyankar, Uriel M., Branford, CT, UNITED STATES
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        Gusev, Vladimir Y., Madison, CT, UNITED STATES
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        Shenoy, Suresh G., Branford, CT, UNITED STATES
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PΙ
        US 2004010119
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20010213 (60)
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        US 2001-268496P
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        US 2001-335104P
        US 2001-335109P
                                20011031 (60)
        US 2001-332127P
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20011121 (60)

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20011121 (60)
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FS
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        INCLM: 530/350.000
        INCLS: 514/012.000; 435/006.000; 435/069.100; 435/320.100; 435/325.000;
                536/023.200
                530/350.000
NCL
        NCLM:
                514/012.000; 435/006.000; 435/069.100; 435/320.100; 435/325.000;
        NCLS:
                536/023.200
        [7]
IC
        ICM: C12Q001-68
        ICS: C07H021-04; A61K038-17; C07K014-435; C07K014-47; C12P021-02;
        C12N005-06
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
12
      ANSWER 9 OF 156 CAPLUS COPYRIGHT 2004 ACS ON STN DUPLICATE 5
      2004:539519 CAPLUS
AN
                                                 ***Grb14***
      Regulation and functional roles of
ΤI
      Cariou, Bertrand; Bereziat, Veronique; Moncoq, Karine; Kasus-Jacobi, Anne;
ΑU
      Perdereau, Dominique; Le Marcis, Veronique; Burnol, Anne-Francoise
      Dep. Endocrinol., Inst. Cochin INSERM U 567-CNRS UMR 8104, Univ. Rene
CS
      Descartes, Paris, 75014, Fr.
Frontiers in Bioscience (2004), 9(2), 1626-1636
SO
      CODEN: FRBIF6; ISSN: 1093-4715
      URL: http://www.bioscience.org/2004/v9/af/1228/pdf.pdf
PR
      Frontiers in Bioscience
      Journal; (online computer file)
DT
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LA
      ANSWER 10 OF 156 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
L2
      2004:240131 SCISEARCH
AN
      The Genuine Article (R) Number: 779ZA
GA
      Regulation and functional roles of ***Grb14***
ΤI
      Cariou B; Bereziat V; Moncoq K; Kasus-Jacobi A; Perdereau D; Le Marcis V;
ΑU
      Burnol A F (Reprint)
      Univ Paris 05, CNRS, UMR 8104, Dept Endocrinol, INSERM, U567, Inst Cochin, F-75014 Paris, France (Reprint); Fac Pharm Paris V, Lab Cristallog & RMN
CS
      Biol, F-75006 Paris, France
CYA
      FRONTIERS IN BIOSCIENCE, (MAY 2004) Vol. 9, pp. 1626-1636.
      Publisher: FRONTIERS IN BIOSCIENCE INC, C/O NORTH SHORE UNIV HOSPITAL,
      BIOMEDICAL RESEARCH CENTER, 350 COMMUNITY DR, MANHASSET, NY 11030 USA.
      ISSN: 1093-9946.
      Article; Journal
DT
      English
LA
REC
      Reference Count: 86
      *ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS*
L2
      ANSWER 11 OF 156 CAPLUS COPYRIGHT 2004 ACS ON STN
      2004:471136 CAPLUS
AN
TI
      Increased adipose tissue expression of
                                                      ***Grb14***
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      of insulin resistance
      Carfiou, Bertrand; Capitaine, Nadege; Le Marcis, Veronique; Vega
AU
     Nathalie; Bereziat, Veronique; Kergoat, Micheline; Laville, Martine; Girard, Jean; Vidal, Hubert; Burnol, Anne-Francoise Dep. d'Endocrinol., Inst. Cochin INSERUM U 567-CNRS UMR 8104, Univ. Rene Descartes, Paris, 75674, Fr. FASEB Journal (2004), 18(9), 965-967, 10.1096/fj.03-0824fje CODEN: FAJOEC; ISSN: 0892-6638 Federation of American Societies for Experimental Biology
CS
SO
PB
DT
      Journal
      English
LA
RE.CNT 36
                THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD
                ALL CITATIONS AVAILABLE IN THE RE FORMAT
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                              MEDLINE on STN
      2004279843
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AN
      PubMed ID: 15059968
DN
TI
      Increased adipose tissue expression of
                                                    ***Grb14***
                                                                      in several models
      of insulin resistance.
      Cariou Bertrand; Capitaine Nadege; Le Marcis Veronique; Vega Nathalie;
      Bereziat Veronique; Kergoat Micheline; Laville Martine; Girard Jean; Vidal
      Hubert; Burnol Anne-Francoise
      Departement d'Endocrinologie, Institut Cochin INSERM U 567-CNRS UMR
CS
```

8104-Universite Rene Descartes, Paris, France.

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S0
     FASEB journal : official publication of the Federation of American
     Societies for Experimental Biology, (2004 Jun) 18 (9) 965-7.
     Journal code: 8804484. ISSN: 1530-6860.
     United States
CY
     Journal; Article; (JOURNAL ARTICLE)
DT
LA
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FS
     IN-PROCESS; NONINDEXED; Priority Journals
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     Last Updated on STN: 20040608
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     ANSWER 13 OF 156 CAPLUS COPYRIGHT 2004 ACS ON STN DUPLICATE 6
     2004:114768 CAPLUS
AN
     140:315199
DN
     Grb10 exceeding the boundaries of a common signaling adapter
     Riedel, Heimo
ΑU
     Department of Biological Sciences, Wayne State University, Detroit, MI,
     48202, USA
     Frontiers in Bioscience (2004), 9(1), 603-618
50
     CODEN: FRBIF6; ISSN: 1093-4715
     URL: http://www.bioscience.org/2004/v9/af/1227/pdf.pdf
PB
     Frontiers in Bioscience
     Journal; General Review; (online computer file)
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CS
     (Reprint); Wayne State Univ, Dept Biol Sci, Detroit, MI 48202 USA
CYA
     FRONTIERS IN BIOSCIENCE, (JAN 2004) Vol. 9, pp. 603-618. Publisher: FRONTIERS IN BIOSCIENCE INC, C/O NORTH SHORE UNIV HOSPITAL,
S0
     BIOMEDICAL RESEARCH CENTER, 350 COMMUNITY DR, MANHASSET, NY 11030 USA.
     ISSN: 1093-9946.
DT
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REC
     Reference Count: 105
     *ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS*
L2
     ANSWER 15 OF 156 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
     DUPLICATE 7
     2004:244934
                   BIOSIS
     PREV200400246629
DN
TT
     Improved glucose homeostasis and enhanced insulin signalling in
        ***Grb14*** -deficient mice.
     Cooney, Gregory J.; Lyons, Ruth J.; Crew, A. Jayne; Jensen, Thomas E.;
     Molero, Juan Carlos; Mitchell, Christopher J.; Biden, Trevor J.; Ormandy,
     Christopher J.; James, David E.; Daly, Roger J. [Reprint Author]
     Cancer Research Program, Garvan Institute of Medical Research, 384
CS
     Victoria St, Sydney, NSW, 2010, Australia
     r.daly@garvan.org.au
     EMBO (European Molecular Biology Organization) Journal, (11 February 2004) Vol. 23, No. 3, pp. 582-593. print. ISSN: 0261-4189 (ISSN print).
S0
     Article
     English
ED
     Entered STN: 6 May 2004
     Last Updated on STN: 6 May 2004
L2
     ANSWER 16 OF 156 CAPLUS COPYRIGHT 2004 ACS ON STN DUPLICATE 8
     2004:114729 CAPLUS
AN
DN
     140:214448
TT
     Grb10: more than a simple adaptor protein
     Lim, Mei A.; Riedel, Heimo; Liu, Feng
ΑU
     Department of Pharmacology, University of Texas Health Science Center at
     San Antonio, San Antonio, TX, 78229, USA
Frontiers in Bioscience (2004), 9(1), 387-403
S0
     CODEN: FRBIF6; ISSN: 1093-4715
     URL: http://www.bioscience.org/2004/v9/af/1226/pdf.pdf
PB
     Frontiers in Bioscience
     Journal; General Review; (online computer file)
DT
     English
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THERE ARE 103 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE.CNT 103
                ALL CITATIONS AVAILABLE IN THE RE FORMAT
L2
      ANSWER 17 OF 156 CAPLUS COPYRIGHT 2004 ACS ON STN DUPLICATE 9
ΑN
      2004:114784 CAPLUS
DN
      140:160771
      GRB7 in intracellular signaling and its role in cell regulation
TI
AU
     Shen, Tang-Long; Guan, Jun-Lin
     Department of Molecular Medicine, Cornell University, Ithaca, NY, 14853,
CS
      USA
      Frontiers in Bioscience (2004), 9(1), 192-200
S0
      CODEN: FRBIF6; ISSN: 1093-4715
      URL: http://www.bioscience.org/2004/v9/af/1229/pdf.pdf
PB
      Frontiers in Bioscience
DT
      Journal; General Review; (online computer file)
      English
LA
RE.CNT 86
                THERE ARE 86 CITED REFERENCES AVAILABLE FOR THIS RECORD
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     ANSWER 18 OF 156 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
L2
      2004:282607 BIOSIS
AN
      PREV200400277875
DN
TI
      Increased adipose tissue expression of
                                                   ***Grb14***
                                                                   in several models
      of insulin resistance.
     Cariou, Bertrand; Capitaine, Nadege; Le Marcis, Veronique; Vega, Nathalie; Bereziat, Veronique; Kergoat, Micheline; Laville, Martine; Girard, Jean; Vidal, Hubert; Burnol, Anne- Françoise [Reprint Author]
ΑU
      CNRSUMR 8104INSERM, U567, Inst Cochin, Dept Endocrinol, Univ Paris 05,
CS
      F-75674, Paris, France
      burnol@cochin.inserm.fr
SO
     FASEB Journal, (April 2004) Vol. 18, No. 6, pp. NIL_0336-NIL_0356. print.
      ISSN: 0892-6638 (ISSN print).
DT
     Article
     English
LA
     Entered STN: 9 Jun 2004
ED
     Last Updated on STN: 9 Jun 2004
L2
     ANSWER 19 OF 156 SCISEARCH COPYRIGHT 2004 THOMSON ISI ON STN
AN
     2004:415366 SCISEARCH
     The Genuine Article (R) Number: 816KM
GΑ
                                                   ***Grb14***
TI
     Increased adipose tissue expression of
                                                                   in several models
     of insulin resistance
     Cariou B; Capitaine N; Le Marcis V; Vega N; Bereziat V; Kergoat M; Laville M; Girard J; Vidal H; Burnol A F (Reprint)
ΑU
     Univ Paris 05, CNRS, UMR 8104, INSERM, U567, Inst Cochin, Dept Endocrinol, F-75674 Paris, France (Reprint); Fac Med R Laennec, Ctr Rech & Nutr
CS
     Humaine Lyon, Lyon, France; Hop Edouard Herriot, Serv Endocrinol Diabetol
     & Nutr, Lyon, France
CYA
     France
SO
     FASEB JOURNAL, (APR 2004) Vol. 18, No. 6.
     Publisher: FEDERATION AMER SOC EXP BIOL, 9650 ROCKVILLE PIKE, BETHESDA, MD
     20814-3998 USA.
     ISSN: 0892-6638.
DT
     Article; Journal
LA
     English
REC
     Reference Count: 36
     *ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS*
L2
     ANSWER 20 OF 156 DISSABS COPYRIGHT (C) 2004 ProQuest Information and
     Learning Company; All Rights Reserved on STN
AN
     2003:43622 DISSABS
                              Order Number: AAI3075524
TI
     Structural and functional analysis of the BPS and SH2 domains of Grb10
ΑU
     Stein, Evan Gary [Ph.D.]; Hubbard, Stevan R. [advisor]
     New York University (0146)
     Dissertation Abstracts International, (2003) Vol. 63, No. 12B, p. 5687. Order No.: AAI3075524. 91 pages.
SO
     ISBN: 0-493-95827-4.
DT
     Dissertation
FS
     DAI
LA
     English
L2
      ANSWER 21 OF 156 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN
      DUPLICATE 10
      2004-01504 BIOTECHDS
ΤI
      Screening for drugs using altered expression of specified genes in
```

frontal lobe or hippocampus of depression model animal, and diagnosis of

```
depression;
            animal model and biochip for use in drug screening and disease therapy
PA
        RIKAGAKU KENKYUSHO
        JP 2003274949 30 Sep 2003
PΙ
        JP 2002-81502 22 Mar 2002
ΑI
        JP 2002-81502 22 Mar 2002; JP 2002-81502 22 Mar 2002
PRAI
DT
        Patent
LA
        Japanese
        WPI: 2003-822458 [77]
os
      ANSWER 22 OF 156 IFIPAT COPYRIGHT 2004 IFI on STN DUPLICATE 11
L2
        10399185 IFIPAT; IFIUDB; IFICDB
ΑN
        DIAGNOSIS OF DISEASES ASSOCIATED WITH THE IMMUNE SYSTEM BY DETERMINING
TI
        CYTOSINE METHYLATION
ΙN
        Berlin Kurt (DE); Olek Alexander (DE); Piepenbrock Christian (DE)
        Unassigned Or Assigned To Individual (68000)
PA
PΙ
        us 2003143606
                            A1 20030731
        us 2002-311455
                                  20021216
ΑI
        WO 2001-EP7537
                                  20010702
                                  20021216
                                               PCT 371 date
                                  20021216
                                               PCT 102(e) date
PRAI
       DE 2000-10032529
                                  20000630
        DE 2000-10043826
                                  20000901
FΙ
        US 2003143606
                                  20030731
DT
        Utility; Patent Application - First Publication
FS
        CHEMICAL
        APPLICATION
CLMN
L2
      ANSWER 23 OF 156 IFIPAT COPYRIGHT 2004 IFI on STN DUPLICATE 12
        10385219 IFIPAT; IFIUDB; IFICDB
ΑN
TI
        GDU, A NOVEL SIGNALLING PROTEIN
        Daly Roger John (AU); Sutherland Robert Lyndsay (AU)
Unassigned Or Assigned To Individual (68000)
US 2003129639 A1 20030710
IN
PA
ΡI
        US 2002-323001
ΑI
                                  20021218
        WO 1996-AU258
RLI
                                  19960502 Section 371 PCT Filing UNKNOWN
        US 1998-945771
                                  19980422 DIVISION
        US 2002-242332
                                  20020911 DIVISION
        AU 1995-2742
PRAI
                                  19950502
        us 2003129639
                                  20030710
FΙ
        us 6465623
        Utility; Patent Application - First Publication
DT
FS
        CHEMICAL
        APPLICATION
CLMN
         3 Figure(s).
GΙ
                                                                 ***Grb14***
      FIG. 1 shows a schematic representation of
                                                                                    structure with
        a restriction map for the ***Grb14*** cDNA and the cDNA clones used to derive the ***Grb14*** sequence aligned underneath. The initial
        clone isolated by CORT screening was designated clone 1. Two other clones (1-1 and 1-2) were isolated from the 184 cell line library by screening
        using clone 1 as a probe. The ***Grb14*** CDNA sequence was completed using two clones L5 and L6, isolated from a human liver cDNA library.
                                                ***Grb14***
        Abbreviations are as follows: A; Apa I; Av; Avr II, X; Xho I; E; Eco RI.
      The numbers refer to distance in bp.

FIG. 2 shows the nucleotide and amino acid sequence of ***Grb14***

The PH domain is underlined and the SH2 domain indicated by bold type.
        The translation termination codon is shown by an asterisk in the amino
        acid sequence. Numbers refer to distances in bp.
      FIG. 3 shows the sequence homology between
        IG. 3 shows the sequence homology between ***Grb14***, Grb7, Grb10 and F10E9.6. As alignment of the amino acid sequences of ***Grb14***
        mouse Grb7, mouse Grb10 and C. elegans F10E9.6 was obtained using the
       computer programs Clustal W and SeqVu. Identical residues are boxed. A highly conserved proline-rich motif is indicated by the dotted underline, the PH domain by the broken underline and the SH2 domain by the bold underline. Only the central region of F10E9.6 exhibiting homology with the Grb7 family is shown. Amino acid residues for each protein are
        numbered (from the initiation methionine) on the right.
L2
      ANSWER 24 OF 156 IFIPAT COPYRIGHT 2004 IFI on STN DUPLICATE 13
ΑN
       10360583 IFIPAT; IFIUDB; IFICDB
TI
       METHODS AND COMPOSITIONS FOR INHIBITING GRB7; ADMINISTERING A
       NON-PHOSPHORYLATED TRIPEPTIDES
       Krag David N; Oligino Lyn; Pero Stephanie C
ΙN
        Unassigned Or Assigned To Individual (68000)
PA
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us 2003105000
                          A1 20030605
       US 2001-13815
                               20011105
      US 2000-245755P
PRAI
                               20001103 (Provisional)
       US 2003105000
                               20030605
       Utility; Patent Application - First Publication
       CHEMICAL
       APPLICATION
CLMN
       93
        16 Figure(s).
      FIG. 1 is a histogram showing the binding of Grb7 binding peptides (G7BP)
       to the SH2 domain of human Grb7 by ELISA.
      FIG. 2 is a histogram showing the binding of a control phage clone to the
       SH2 domain of Grb2 but not to the SH2 domain of Grb7.
      FIG. 3 is a histogram showing the effect of mutation on a G7BP-4 phage clone on its ability to bind to the SH2 domain of Grb7.
FIG. 4 is a histogram showing the binding specificity of seven Grb7
       binding peptides to the SH2 domains of Grb7, Grb7 beta D5beta D6,
                        , full length Grb2, and BSA using a phage ELISA.
          ***Grb14***
      FIG. 5A is a graph showing the inhibition of G7-18 peptide-phage binding
      to Grb7-SH2 with the free synthetic peptides G7-18, G718NATE and G7-8. FIG. 5B is a graph showing the inhibition of G7-8NA peptidephage binding
      to Grb7-SH2 with the free synthetic peptides G7-8, G7-8NA and G7-8NATE. FIG. 6A is a graph showing G7-18NATE inhibits the association of Grb7 with the ErbB family of receptors, as detected by antiphosphotyrosine. FIG. 6B is a densitometric analysis of autoradiographs using the Biorad
       Fluor-S Multimager with Quantity One 4.2.1 software, showing G7-18NATE inhibits the association of Grb7, not Grb2, with the ErbB family in a
       dose-dependent manner.
      FIG. 7A is a graph showing that G7-18NATE inhibits the association of Grb7
       with ErbB3 specifically in a dose-dependent manner, as detected by
       anti-ErbB3 FIG. 7B is a densitometric analysis of autoradiographs using
       the Biorad Fluor-S Multimager with Quantity One 4.2.1 software showing
       that G7-18NATE inhibits the association of Grb7 with ErbB3 in a
       dose-dependent manner.
      FIG. 8A is a graph showing that G7-18NATE inhibits the association of Grb7
       with ErbB2 specifically in a dose-dependent manner, as detected by
       anti-ErbB2.
      FIG. 8B is a densitometric analysis of autoradiographs using the Biorad
       Fluor-S Multimager with Quantity One 4.2.1 software showing that
       G7-18NATE inhibits the association of Grb7 with ErbB2 in a dose-dependent
       manner.
      FIG. 9A is one possible chemical structure for G7BP-4NATE (SEQ ID NO:50).
       Other thioether linkages are illustrated in FIGS. 9B, 9C, 9D and 9E, and
       it is to be understood that any of these linkages can be used in the
       formation of G7BP-4NATE.
      FIG. 9B is the structure of a thioether containing peptide (G1TE) . This
       structure illustrates one possible thioether linkage between the N and C
       terminals of a peptide that can be used in the thioether containing
       peptides of the invention.
      FIG. 9C is another possible structure for the thioether containing peptide
       GI TE. This structure illustrates one possible thioether linkage between
       the N and C terminals of a peptide that can be used in the thioether
       containing peptides of the invention.
      FIG. 9D is another possible structure for the thioether containing peptide
       GITE. This structure illustrates one possible thioether linkage between
      the N and C terminals of a peptide that can be used in the thioether containing peptides of the invention.
FIG. 9E is another possible structure for the thioether containing peptide
       GI TE. This structure illustrates one possible thioether linkage between
       the N and C terminals of a peptide that can be used in the thioether
       containing peptides of the invention.
      ANSWER 25 OF 156 IFIPAT COPYRIGHT 2004 IFI on STN DUPLICATE 14
       10300425 IFIPAT; IFIUDB; IFICDB
       GDU, A NOVEL SIGNALLING PROTEIN; NUCLEOTIDE SEQUENCES CODING POLYPEPTIDE FOR USE IN THE DIAGNOSIS, TREATMENT AND PREVENTION OF CANCER
       Daly Roger John (AU); Sutherland Robert Lyndsay (AU)
       Unassigned Or Assigned To Individual (68000)
       US 2003044834 A1 20030306
       US 2002-242332
                               20020911
       WO 1996-AU258
                               19960502 Section 371 PCT Filing UNKNOWN
                               19980422 DIVISION
       US 1998-945771
                                                                      6465623
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      AU 1995-2742
PRAI
       US 2003044834
                               20030306
       US 6465623
```

Utility; Patent Application - First Publication

PΙ

ΑI

FI

DT FS

GΙ

L2

ΑN

TI

IN

PA

PΙ ΑI

RLI

FΙ

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APPLICATION
CLMN
        3 Figure(s).
GI
                                                              ***Grb14***
      FIG. 1 shows a schematic representation of
                                                                                structure with
       a restriction map for the ***Grb14***
to derive the ***Grb14*** sequence a
                                                           cDNA and the cDNA clones used
                                            sequence aligned underneath. The initial
       clone isolated by CORT screening was designated clone 1. Two other clones (1-1 and 1-2) were isolated from the 184 cell line library by screening
                                              ***Grb14***
       using clone 1 as a probe. The
                                                               cDNA sequence was completed
       using two clones L5 and L6, isolated from a human liver cDNA library.
       Abbreviations are as follows: A; Apa I; Av; Avr II, X; Xho I; E; Eco RI.
       The numbers refer to distance in bp.
      FIG. 2 shows the nucleotide and amino acid sequence of
                                                                             ***Grb14***
       The PH domain is underlined and the SH2 domain indicated by bold type.
       The translation termination codon is shown by an asterisk in the amino
       acid sequence. Numbers refer to distances in bp.
       IG. 3 shows the sequence homology between ***Grb14*** , Grb7, Grb10 and F10E9.6. As alignment of the amino acid sequences of ***Grb14***
                                                              ***Grb14***
      FIG. 3 shows the sequence homology between
       mouse Grb7, mouse Grb10 and C. elegans F10E9.6 was obtained using the
       computer programs Clustal W and SeqVu. Identical residues are boxed. A highly conserved proline-rich motif is indicated by the dotted underline,
       the PH domain by the broken underline and the SH2 domain by the bold underline. Only the central region of F10E9.6 exhibiting homology with the Grb7 family is shown. Amino acid residues for each protein are
       numbered (from the initiation methionine) on the right.
L2
      ANSWER 26 OF 156 USPATFULL ON STN
        2003:330145 USPATFULL
ΑN
        Skin cell biomarkers and methods for identifying biomarkers using
ΤI
        nucleic acid microarrays
IN
        Dooley, Thomas P., Vestavia Hills, AL, UNITED STATES
        Curto, Ernest V., Huntsville, AL, UNITED STATES
        Davis, Richard L., JR., Homewood, AL, UNITED STATES US 2003232356 A1 20031218 US 2003-361006 A1 20030210 (10)
PΙ
ΑI
        US 2002-354519P
                                 20020208 (60)
PRAI
        Utility
DT
FS
        APPLICATION
LN.CNT 1897
        INCLM: 435/006.000
INCL
        INCLS: 702/020.000
        NCLM: 435/006.000
NCL
        NCLS: 702/020.000
IC
         [7]
        ICM: C12Q001-68
        ICS: G06F019-00; G01N033-48; G01N033-50
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
L2
      ANSWER 27 OF 156 USPATFULL ON STN
        2003:225702 USPATFULL
ΑN
        Polynucleotide encoding a novel pleckstrin homology domain and proline
ΤI
        rich domain containing adapter protein, PMN29
        Finger, Joshua N., San Marcos, CA, UNITED STATES
Perez-Villar, Juan J., Mercerville, NJ, UNITED STATES
IN
        Rajashekar, Reddy, Langhorne, PA, UNITED STATES
Yang, Guchen, Morrisville, PA, UNITED STATES
Kiener, Peter A., Doylestown, PA, UNITED STATES
        US 2003157514
                                      20030821
PΙ
                               Αĺ
        US 2002-234816
                                      20020904 (10)
ΑI
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PRAI
        US 2001-317063P
                                 20010904 (60)
        Utility
DT
        APPLICATION
FS
LN.CNT 13865
        INCLM: 435/006.000
INCL
        INCLS: 435/069.100; 435/320.100; 435/325.000; 530/350.000; 536/023.500;
                 435/007.200
NCL
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                 435/006.000
        NCLS:
                 435/069.100; 435/320.100; 435/325.000; 530/350.000; 536/023.500;
                 435/007.200
        [7]
IC
        ICM: C12Q001-68
        ICS: G01N033-53; G01N033-567; C07H021-04; C12P021-02; C12N005-06;
        C07K014-47
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
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FS

CHEMICAL

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L2
     ANSWER 28 OF 156 USPATFULL ON STN
ΑN
       2003:37578 USPATFULL
TT
       Specimen-linked G protein coupled receptor database
       Muraca, Patrick J., Pittsfield, MA, UNITED STATES
IN
PΤ
       us 2003027223
                           Α1
                                20030206
       US 2002-184694
                                20020628 (10)
ΑI
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       US 2001-302316P
                            20010629 (60)
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DT
FS
       APPLICATION
LN.CNT 3618
INCL
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       INCLS: 702/019.000
              435/007.210
NCL
       NCLM:
       NCLS:
              702/019.000
       [7]
IC
       ICM: G01N033-567
       ICS: G06F019-00; G01N033-48; G01N033-50
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
L2
     ANSWER 29 OF 156 USPATFULL on STN
       2003:222015 USPATFULL
ΑN
       Compositions for the detection of blood cell and immunological response
TI
       gene expression
IN
       Cocks, Benjamin G., Sunnyvale, CA, United States
       Stuart, Susan G., Montara, CA, United States
Seilhamer, Jeffrey J., Los Altos Hills, CA, United States
       Incyte Corporation, Palo Alto, CA, United States (U.S. corporation)
PΑ
                           в1
PΙ
       US 6607879
                                20030819
       us 1998-23655
                                19980209 (9)
ΑI
DT
       Utility
FS
       GRANTED
LN.CNT 3719
INCL
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       INCLS: 435/069.100; 536/023.100; 536/024.100; 536/024.300; 536/024.310;
               536/024.320; 536/024.330
NCL
       NCLM:
               435/006.000
       NCLS:
              435/069.100; 536/023.100; 536/024.100; 536/024.300; 536/024.310;
               536/024.320; 536/024.330
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       ICM: C120001-68
       ICS: C07H021-00
EXF
       435/6; 435/69.1; 536/22.1; 536/23.1; 536/24.1; 536/24.3-24.33
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
     ANSWER 30 OF 156 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
L2
     DUPLICATE 15
     2003:254017
ΑN
                  BIOSIS
     PREV200300254017
DN
ΤI
     Structural basis for dimerization of the Grb10 Src homology 2 domain.
     Implications for ligand specificity.
     Stein, Evan G.; Ghirlando, Rodolfo; Hubbard, Stevan R. [Reprint Author]
ΑU
CS
     Skirball Institute of Biomolecular Medicine, New York University School of
     Medicine, 540 First Ave., New York, NY, 10016, USA
     hubbard@saturn.med.nyu.edu
     Journal of Biological Chemistry, (April 11 2003) Vol. 278, No. 15, pp.
S<sub>0</sub>
     13257-13264. print.
     CODEN: JBCHA3. ISSN: 0021-9258.
DT
     Article
     English
LA
FD
     Entered STN: 28 May 2003
     Last Updated on STN: 28 May 2003
L2
     ANSWER 31 OF 156 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
     DUPLICATE 16
     2003:355616
                  BIOSIS
DN
     PREV200300355616
TI
     NIK is a component of the EGF/herequlin receptor signaling complexes.
ΑU
     Chen, Danying; Xu, Liang-Guo; Chen, Lei; Li, Lixia; Zhai, Zhonghe; Shu,
     Hong-Bing [Reprint Author]
CS
     Department of Immunology, National Jewish Medical and Research Center
     University of Colorado Health Sciences Center, 1400 Jackson Street, K516c,
     Denver, CO, 80206, USA
     shuh@njc.org
     Oncogene, (10 July 2003) Vol. 22, No. 28, pp. 4348-4355. print.
S0
     ISSN: 0950-9232 (ISSN print).
     Article
DT
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English
      Entered STN: 6 Aug 2003
ED
      Last Updated on STN: 6 Aug 2003
      ANSWER 32 OF 156 LIFESCI
                                          COPYRIGHT 2004 CSA on STN
L2
      2003:53872 LIFESCI
AN
TI
      The Grb10/Nedd4 Complex Regulates Ligand-Induced Ubiquitination and
      Stability of the Insulin-Like Growth Factor I Receptor
ΑU
      Vecchione, A.; Marchese, A.; Henry, P.; Rotin, D.; Morrione, A.*
      Department of Urology and Kimmel Cancer Center, Thomas Jefferson
CS
      University, BLSB Room 631, 233 South 10th St., Philadelphia, PA 19107; E-mail: Andrea.Morrione@mail.tju.edu
      Molecular and Cellular Biology [Mol. Cell. Biol.], (20030500) vol. 23, no.
SO
      9, pp. 3363-3372. ISSN: 0270-7306.
      Journal
DT
FS
      English
LA
SL
      English
       ANSWER 33 OF 156 DRUGU COPYRIGHT 2004 THOMSON DERWENT ON STN
L2
       2004-08282 DRUGU
                                Р В
AN
TI
       Imatinib_induces mitochondria-dependent apoptosis of the Bcr-Abl-positive
       K562 cell line and its differentiation toward the erythroid lineage.
       Jacquel A; Herrant M; Legros L; Belhacene N; Luciano F; Pages G; Hofman
ΑU
       P; Auberger P
       Nice, Fr.
10
       FASEB J. (17, No. 14, 2160-62, 2003) 3 Fig.
S0
       CODEN: FAJOEC
                                ISSN: 0892-6638
       INSERM U526, Physiopathologie de la Survie et de la Mort Cellulaires et
       Infections Virales Equipe Labellisee par la LNC, 06107 Nice-Cedex 2,
       France. (P.A.). (e-mail: auberger@unice.fr).
LA
       English
       Journal
DT
       AB; LA; CT
FΑ
FS
       Literature
      ANSWER 34 OF 156 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
L2
AN
      2003:476188 BIOSIS
DN
      PREV200300476188
      Characterization of a novel gene (HGP1) potentially involved in
TI
      osteosarcoma progression.
     Eppert, Kolja [Reprint Author]; Aneliunas, Vicky [Reprint Author]; Wunder, Jay S. [Reprint Author]; Andrulis, Irene L. [Reprint Author] Fred A. Litwin Centre for Cancer Genetics, Samuel Lunenfeld Research Institute, Mount Sinai Hospital, Toronto, ON, Canada Proceedings of the American Association for Cancer Research Annual Meeting, (July 2003) Vol. 44, pp. 1041-1042. print.

Meeting Info.: 94th Annual Meeting of the American Association for Cancer
ΑU
SO
      Research. Washington, DC, USA. July 11-14, 2003.
      ISSN: 0197-016x.
      Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
DT
      Enalish
ED
      Entered STN: 15 Oct 2003
      Last Updated on STN: 15 Oct 2003
L2
      ANSWER 35 OF 156 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
      DUPLICATE 17
ΑN
      2004:49749 BIOSIS
DN
      PREV200400053388
TI
      Using gene expression profiling to identify the molecular basis of the
      synergistic actions of hepatocyte growth factor and vascular endothelial
      growth factor in human endothelial cells.
      Gerritsen, Mary E. [Reprint Author]; Tomlinson, James E.; Zlot, Constance; Ziman, Michael; Hwang, Stuart 541 Parrott Drive, San Mateo, CA, 94402, USA
ΑU
CS
      meg570@comcast.net
      British Journal of Pharmacology, (October 2003) Vol. 140, No. 4, pp.
SO
      595-610. print.
      ISSN: 0007-1188 (ISSN print).
DT
      Article
      English
LA
      Entered STN: 21 Jan 2004
ED
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Last Updated on STN: 21 Jan 2004

L2 ANSWER 36 OF 156 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN DUPLICATE 18 2003:451765 BIOSIS AN PREV200300451765 DN Carcinogen mediated initiation of glial progenitors in the rat brain TI results in marked dependency of proliferation and differentiation by insulin and FGF-2. Kokkinakis, Demetrius Michael [Reprint Author]; Yang, Shuting [Reprint ΑIJ Authorl CS University of Pittsburgh, Pittsburgh, PA, USA Proceedings of the American Association for Cancer Research Annual SO Meeting, (July 2003) Vol. 44, pp. 482. print. Meeting Info.: 94th Annual Meeting of the American Association for Cancer Research. Washington, DC, USA. July 11-14, 2003. ISSN: 0197-016X. Conference; (Meeting)
Conference; Abstract; (Meeting Abstract) DT English Entered STN: 1 Oct 2003 FD Last Updated on STN: 1 Oct 2003 ANSWER 37 OF 156 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN L2 DUPLICATE 19 2003:587917 BIOSIS AN PREV200300570714 DN The PIR domain of ***Grb14*** is an intrinsically unstructured TI protein: Implication in insulin signaling. Moncoq, Karine; Broutin, Isabelle [Reprint Author]; Larue, Valery; Perdereau, Dominique; Cailliau, Katia; Browaeys-Poly, Edith; Burnol, Anne-Francoise; Ducruix, Arnaud Laboratoire de Cristallographie et RMN Biologiques, Faculte de Pharmacie Paris 5, 4 avenue de l'observatoire, 75270, Paris Cedex, 06, France broutin@pharmacie.univ-paris5.fr FEBS Letters, (20 November 2003) Vol. 554, No. 3, pp. 240-246. print. SO. CODEN: FEBLAL. ISSN: 0014-5793. Article LA English Entered STN: 10 Dec 2003 ED Last Updated on STN: 10 Dec 2003 ANSWER 38 OF 156 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN L2 DUPLICATE 20 2003:390017 BIOSIS AN PREV200300390017 DN Inhibition of FGF receptor signalling in Xenopus oocytes: Differential TT effect of Grb7, Grb10 and ***Grb14*** Cailliau, Katia; Le Marcis, Veronique; Bereziat, Veronique; Perdereau, Dominique; Cariou, Bertrand; Vilain, Jean Pierre; Burnol, Anne-Francoise; ΑU Browaeys-Poly, Edith [Reprint Author] Laboratoire de Biologie du Developpement, Universite des Sciences; CS Technologies de Lille, UPRES UA 1033, IFR 118, Batiment SN3, Villeneuve d'Ascq Cedex, France edith.browaeys@univ-lille1.fr FEBS Letters, (31 July 2003) Vol. 548, No. 1-3, pp. 43-48. print. CODEN: FEBLAL. ISSN: 0014-5793. SO Article English LA Entered STN: 27 Aug 2003 ED Last Updated on STN: 27 Aug 2003 L2 ANSWER 39 OF 156 DISSABS COPYRIGHT (C) 2004 ProQuest Information and Learning Company: All Rights Reserved on STN Order Number: AAIMQ78889 ΑN 2004:5360 DISSABS Mitochondrial membrane binding and protein complexing of the TI anti-apoptotic adaptor protein Grb10 Hassard, Jennifer L. [M.Sc.]; Thomas, David [advisor] ΑU McGill University (Canada) (0781) Masters Abstracts International, (2002) Vol. 41, No. 6, p. 1674. Order No.: AAIMQ78889. 75 pages. CS S0 ISBN: 0-612-78889-X. DT Dissertation FS MAI English LA ED Entered STN: 20040107 Last Updated on STN: 20040107

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ANSWER 40 OF 156 CAPLUS COPYRIGHT 2004 ACS ON STN DUPLICATE 21
L2
     2002:285562 CAPLUS
AN
DN
     137:61578
     Expressed gene sets as markers for specific tumors
TI
     Ramaswamy, Sridhar; Golub, Todd B.; Tamayo, Pablo; Angelo, Michael
IN
     Whitehead Institute for Biomedical Research, USA; Dana-Farber Cancer
PA
     Institute, Inc.
S0
     PCT Int. Appl., 715 pp.
     CODEN: PIXXD2
DT
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     English
LA
FAN.CNT 4
                        KIND DATE
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                                                                   DATE
     PATENT NO.
     wo 2002024956
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PRAI US 2000-233534P
     US 2001-278749P
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     wo 2001-US29287
                               20010919
                         W
L2
     ANSWER 41 OF 156 IFIPAT COPYRIGHT 2004 IFI on STN DUPLICATE 22
ΑN
                 IFIPAT;IFIUDB;IFICDB
      GDU, A NOVEL SIGNALLING PROTEIN; IT MAY PROVIDE A TARGET IN DISEASES OR
TI
      CONDITIONS IN WHICH PLATELET DERIVED GROWTH FACTOR RECEPTOR (PDGFR) PLAYS
      A REGULATORY ROLE E.G. WOUND HEALING, FIBROTIC CONDITIONS,
      ATHEROSCLEROSIS
      DALY ROGER JOHN (AU); SUTHERLAND ROBERT LINDSAY (AU)
ΙN
      Unassigned Or Assigned To Individual (68000)
PA
PPA
      Garvan Institute of Medical Research AU (Probable)
                        A1 20020704
PΙ
      us 2002086328
      US 1998-945771
                             19980422
ΑI
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                             19960502
      us 2002086328
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FΙ
      us 6465623
                             20021015
      Utility; Patent Application - First Publication
DT
FS
      CHEMICAL
      APPLICATION
CLMN
GΙ
        3 Figure(s).
                                                       ***Grb14***
     FIG. 1 shows a schematic representation of
                                                                       structure with
      a restriction map for the
                                    ***Grb14***
                                                     cDNA and the cDNA clones used
                        ***Grb14*** sequence aligned underneath. The initial
      to derive the
      clone isolated by CORT screening was designated clone 1. Two other clones (1-1 and 1-2) were isolated from the 184 cell line library by screening
      using clone_1 as a probe. The _ ***Grb14***
                                                         cDNA sequence was completed
      using two clones L5 and L6, isolated from a human liver cDNA library.
      Abbreviations are as follows: A; Apa I; Av; Avr II, X; Xho I; E; Eco RI.
      The numbers refer to distance in bp.
                                                                     ***Grb14***
      FIG. 2 shows the nucleotide and amino acid sequence of
      The PH domain is underlined and the SH2 domain indicated by bold type.
      The translation termination codon is shown by an asterisk in the amino
      acid sequence. Numbers refer to distances in bp.
      and F10E9.6. As alignment of the amino acid sequences of ***Grb14***
     FIG. 3 shows the sequence homology between
      mouse Grb7, mouse Grb10 and C. elegans F10E9.6 was obtained using the
       computer programs Clustal W and SeqVu. Identical residues are boxed. A
```

highly conserved proline-rich motif is indicated by the dotted underline, the PH domain by the broken underline and the SH2 domain by the bold underline. Only the central region of F10E9.6 exhibiting homology with the Grb7 family is shown. Amino acid residues for each protein are numbered (from the initiation methionine) on the right.

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L2
     ANSWER 42 OF 156 IFIPAT COPYRIGHT 2004 IFI on STN DUPLICATE 23
       10094016 IFIPAT; IFIUDB; IFICDB
AN
TI
       POTENTIAL EFFECTOR FOR THE GRB7 FAMILY OF SIGNALLING PROTEINS; NUCLEOTIDE
       SEQUENCES CODING SIGNAL TRANSDUCTION PLYPEPTIDE; FOR USE IN THE DIAGNOSIS
       AND TREATMENT OF CANCERS
       DALY ROGER JOHN (AU); SUTHERLAND ROBERT L (AU)
IN
       Unassigned Or Assigned To Individual (68000)
PΑ
PΙ
       US 2002037582
                         Α1
                              20020328
ΑI
          2000-509196
                               20000323
                               19980923
       wo 1998-AU795
       AU 1997-9388
PRAI
                               19970923
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       us 2002037582
FI
       Utility; Patent Application - First Publication
DT
FS
       CHEMICAL
       APPLICATION
CLMN
       15
        2 Figure(s).
GΙ
      FIG. 1 provides the nucleotide and amino acid (single letter code)
       sequence of 2.2412. Numbers refer to distances in base pairs.
       Ankyrin-type repeat sequences are underlined. An additional repeat sequence is indicated by italics. The stop codon is represented by all asterisk. The original cDNA clone 2. 2412 isolated by the two hybrid
       screen spans nucleotides 6942664 of this sequence.
                                                                        ***Grb14***
      FIG. 2 provides a map of the 2.2412-binding region on
       structure of the deletion constructs used in the analysis. Ga14 DNA-BD
                                                       ***Grb14***
       fusion constructs encoding full length
                                                                        (FL), the
       Nterminal (N), central region (C) and N-terminal+central region (N+C) were generated in the vector pAS2.1. B. Results of betagalactosidase
       activity assays following transformation of the above plasmids into yeast
       strain Y190 together with the original 2.2412 cDNA clone in pACT-2.
      ANSWER 43 OF 156 CAPLUS COPYRIGHT 2004 ACS on STN
L2
      2002:10730 CAPLUS
AN
DN
      136:49326
      Diagnosis of diseases associated with the immune system using oligomer
      probes to detect cytosine methylation state
      Olek, Alexander; Piepenbrock, Christian; Berlin, Kurt
IN
PA
      Epigenomics A.-G., Germany
SO
      PCT Int. Appl., 32 pp.
      CODEN: PIXXD2
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                          KIND DATE
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      wo 2002000928
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961 U1 20040129 DE 2001-
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L2
     ANSWER 44 OF 156
                       USPATFULL on STN
       2002:315083 USPATFULL
AN
       Nucleic acid sequences associated with baldness
TI
       Pritchard, David, Seattle, WA, UNITED STATES
IN
       Burmer, Glenna, Seattle, WA, UNITED STATES
       Brown, Joseph, Seattle, WA, UNITED STATES
              Vasiliki, Seattle, WA, UNITED STATES
2177566 A1 20021128
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LN.CNT 3768
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INCL
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              435/006.000; 435/007.210; 424/070.100
       NCLS:
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       [7]
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       ICS: C12Q001-68; G01N033-567; A61K007-06
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       2002:181561 USPATFULL
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TI
       Process for in vitro selection of high methol producing genotypes
IN
       Khanuja, Suman Preet Singh, Lucknow, INDIA
       Shasany, Ajit Kumar, Lucknow, INDIA
       Dhawan, Sunita, Lucknow, INDIA
       Darokar, Mahendra Pandurang, Lucknow, INDIA
       Kumar, Tiruppadiripuliyur Ranganathan Santha, Lucknow, INDIA
       Saikia, Dharmendra, Lucknow, INDIA
       Naqui, Arif Ali, Lucknow, INDIA
       Kumar, Sushil, Lucknow, INDIA
       Council of Scientific&Industrial Reaearch, New Delhi, INDIA (non-U.S.
PA
       corporation)
       US 6423541
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                                20020723
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DT
FS
       GRANTED
LN.CNT 741
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              435/420.000
NCL
              435/410.000; 435/421.000; 435/430.000; 435/430.100; 435/431.000
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       [7]
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EXF
       435/410; 435/420; 435/421; 435/430; 435/430.1; 435/431
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
L2
                       WPIDS COPYRIGHT 2004 THOMSON DERWENT ON STN
     ANSWER 46 OF 156
     2002-547451 [58]
ΑN
                         WPIDS
     C2002-155181
DNC
     Treatment or prophylaxis of a subject having a disorder characterized by
TI
     abnormal interaction of Grb7 and a Grb7 ligand, involves administering to
     a non-phosphorylated peptide to a subject in need of the treatment.
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B04 D16

DC

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KRAG, D N; OLIGINO, L; PERO, S C (UYVE-N) UNIV VERMONT & STATE AGRIC COLLEGE; (KRAG-I) KRAG D N; (OLIG-I)
TN
     OLIGINO L; (PERO-I) PERO S C
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     23
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                                                        A61K038-00
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                                                         A61K038-17
     wo 2002036142 A2 wo 2001-US47400 20011105; AU 2002020265 A AU 2002-20265
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     20011105; US 2003105000 A1 Provisional US 2000-245755P 20001103, US
     2001-13815 20011105
     AU 2002020265 A Based on WO 2002036142
                                                            20011105
PRAI US 2000-245755P
                           20001103; us 2001-13815
     ICM A61K038-00; A61K038-17
IC
     ANSWER 47 OF 156 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
L2
     DUPLICATE 24
     2002:492206
                  BIOSIS
AN
DN
     PREV200200492206
     Association of Grb7 with phosphoinositides and its role in the regulation
TI
     of cell migration.
     Shen, Tang-Long; Han, Dong Cho; Guan, Jun-Lin [Reprint author]
ΑU
     Department of Molecular Medicine, Cornell University, Ithaca, NY, 14853,
     jg19@cornell.edu
     Journal of Biological Chemistry, (August 9, 2002) Vol. 277, No. 32, pp.
SO
     29069-29077 print.
     CODEN: JBCHA3. ISSN: 0021-9258.
DT
     Article
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LA
     Entered STN: 18 Sep 2002
FD
     Last Updated on STN: 18 Sep 2002
     ANSWER 48 OF 156 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
L2
     DUPLICATE 25
     2002:292126 BIOSIS
     PREV200200292126
DN
     Identification of novel non-phosphorylated ligands, which bind selectively
TT
     to the SH2 domain of Grb7.
     Pero, Stephanie C.; Oligino, Lyn; Daly, Roger J.; Soden, Amy L.; Liu,
     Chen; Roller, Peter P.; Li, Peng; Krag, David N. [Reprint author]
Department of Surgery, University of Vermont School of Medicine, Given
CS
     Medical Building, Rm. E309, Burlington, VT, 05405, USA
     David.Krag@uvm.edu
     Journal of Biological Chemistry, (April 5, 2002) Vol. 277, No. 14, pp.
SO
     11918-11926. print.
     CODEN: JBCHA3. ISSN: 0021-9258.
     Article
DT
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LA
ED
     Entered STN: 15 May 2002
     Last Updated on STN: 15 May 2002
     ANSWER 49 OF 156 CAPLUS COPYRIGHT 2004 ACS on STN
12
AN
     2002:875636 CAPLUS
DN
     138:151170
     Comparative analysis of mutation frequency of coding and non coding short
ΤI
     mononucleotide repeats in mismatch repair deficient colorectal cancers
     Duval, Alex; Reperant, Maryline; Hamelin, Richard
     INSERM U434, CEPH, Paris, Fr.
CS
SO
     Oncogene (2002), 21(52), 8062-8066
     CODEN: ONCNES; ISSN: 0950-9232
PR
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DT
     Journal
     English
LA
               THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD
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     ANSWER 50 OF 156 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
L2
     DUPLICATE 26
     2002:529717
                   BIOSIS
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DN
                                                      and regulates its inhibitory
     The adapter protein ZIP binds
                                       ***Grb14***
TΙ
     action on insulin signaling by recruiting protein kinase Czeta.
     Cariou, Bertrand; Perdereau, Dominique; Cailliau, Katia; Browaeys-Poly,
ΑU
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Edith; Bereziat, Veronique; Vasseur-Cognet, Mireille; Girard, Jean;

Burnol, Anne-Francoise [Reprint author] Departement d'Endocrinologie, Institut Cochin, CNRS-INSERM-Universite Rene CS Descartes, 24 Rue du Faubourg Saint-Jacques, 75674, Paris, France burnol@cochin.inserm.fr Molecular and Cellular Biology, (October, 2002) Vol. 22, No. 20, pp. SO 6959-6970. print. CODEN: MCEBD4. ISSN: 0270-7306. Article DT English LA Entered STN: 16 Oct 2002 ED Last Updated on STN: 16 Oct 2002 ANSWER 51 OF 156 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN L2 **DUPLICATE 27** 2002:207358 **BIOSIS** PREV200200207358 DN Inhibition of insulin receptor catalytic activity by the molecular adapter TI ***Grb14*** Bereziat, Veronique; Kasus-Jacobi, Anne; Perdereau, Dominique; Cariou, ΑU Bertrand; Girard, Jean; Burnol, Anne-Francoise [Reprint author] CS Endocrinologie et Metabolisme, CNRS UPR 1524, Institut Cochin de Genetique Moleculaire, 24 rue du Faubourg Saint-Jacques, 75674, Paris Cedex, 14, France burnol@cochin.inserm.fr Journal of Biological Chemistry, (February 15, 2002) Vol. 277, No. 7, pp. S0 4845-4852. print. CODEN: JBCHA3. ISSN: 0021-9258. DT Article English LA ED Entered STN: 20 Mar 2002 Last Updated on STN: 20 Mar 2002 L2 ANSWER 52 OF 156 CAPLUS COPYRIGHT 2004 ACS on STN 2003:3572 CAPLUS AN DN 138:382650 Ontogeny and the possible function of a novel epidermal growth factor-like repeat domain-containing protein, NELL2, in the rat brain ΔIJ Kim, Hyun; Ha, Chang Man; Choi, Jungil; Choi, Eun Jung; Jeon, Jongrye; Kim, Changmee; Park, Sang Kyu; Kang, Sang Soo; Kim, Kyungjin; Lee, Byung CS Department of Anatomy, Brain Korea 21 Biomedical Sciences, Korea University College of Medicine, Seoul, S. Korea SO Journal of Neurochemistry (2002), 83(6), 1389-1400 CODEN: JONRA9; ISSN: 0022-3042 PB Blackwell Science Ltd. DT Journal English LA 46 RE.CNT THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT L2 ANSWER 53 OF 156 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN 2002:396091 BIOSIS ΑN DN PREV200200396091 TI Gene expression profiling of endometrial carcinomas: Identification of molecular biomarkers. Yap, Oi Wah Stephanie [Reprint author]; Zhu, Shirley [Reprint author]; van de Rijn, Matt [Reprint author]; Longacre, Teri [Reprint author]; Teng, Nelson [Reprint author]; Husain, Amreen [Reprint author] CS Stanford University Medical Center, Stanford, CA, USA Proceedings of the American Association for Cancer Research Annual SO Meeting, (March, 2002) Vol. 43, pp. 746. print. Meeting Info.: 93rd Annual Meeting of the American Association for Cancer Research. San Francisco, California, USA. April 06-10, 2002. ISSN: 0197-016x. Conference; (Meeting)
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     Natl Univ, Coll Med, Dept Anat, Chinju 660280, South Korea
CYA
     South Korea
     NEUROREPORT, (4 MAR 2002) Vol. 13, No. 3, pp. 285-289.
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     Publisher: LIPPINCOTT WILLIAMS & WILKINS, 530 WALNUT ST, PHILADELPHIA, PA
     19106-3621 USA.
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     PREV200300124261
     Assignment of backbone 1H, 13C, and 15N resonances of the SH2 domain of
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             ***Grb14***
ΑU
     Scharf, Paul J.; Lyons, Barbara A. [Reprint Author]
     Department of Biochemistry, College of Medicine, University of Vermont,
CS
     Burlington, VT, 05405, USA
     blyons@zoo.uvm.edu
     Journal of Biomolecular NMR, (November 2002) vol. 24, No. 3, pp. 275-276.
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     Girard J; Burnol A F
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     Publisher: AMER DIABETES ASSOC, 1660 DUKE ST. ALEXANDRIA. VA 22314 USA.
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     Reconfirming of the Differentially Expressed Proteins by Using RT-PCT.
     Li, D. [Reprint Author]; Zhang, Q. J.
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     Ocular Genetics and Molec Bio, Zhonghsan Ophthalmic Ctr, GuanZhou, China
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     Meeting Info.: Annual Meeting of the Association For Research in Vision
     and Ophthalmology. Fort Lauderdale, Florida, USA. May 05-10, 2002.
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     likelihood of baldness and for gene therapy
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     Pritchard, David; Burmer, Glenna; Brown, Joseph; Demas, Vasiliki
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     Lifespan Biosciences, Inc., USA
SO
     PCT Int. Appl., 87 pp.
     CODEN: PIXXD2
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     Lyons, Ruth J.; Deane, Roisin; Lynch, Danielle K.; Ye, Zheng-Sheng
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     Jeffrey; Sanderson, Georgina M.; Eyre, Helen J.; Sutherland, Grant R.;
     Daly, Roger J. [Reprint author]
CS
     Cancer Research Program, Garvan Institute of Medical Research, St.
     Vincent's Hospital, Sydney, NSW, 2010, Australia
     r.daly@garvan.org.au
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     molecules and potential cellular functions.
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     Han, Dong Cho; Shen, Tang-Long; Guan, Jun-Lin [Reprint author]
     Cancer Biology Laboratories, Department of Molecular Medicine, Cornell University, Ithaca, NY, 14853, USA
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     jg19@cornell.edu
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     Ōncogene, (1 October, 2001) Vol. 20, No. 44, pp. 6315-6321. print.
     CODEN: ONCNES. ISSN: 0950-9232.
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     colorectal cancer cell lines
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     Gayet, Jacqueline; Zhou, Xiao-Ping; Duval, Alex; Rolland, Sandra; Hoang,
     Jean-Marc; Cottu, Paul; Hamelin, Richard
     INSERM U434 - CEPH, Paris, 75010, Fr.
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     Evolution of instability at coding and non-coding repeat sequences in
ΤI
     human MSI-H colorectal cancers
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     Duval, Alex; Rolland, Sandra; Compoint, Aurore; Tubacher, Emmanuel;
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      IGF1 receptors.
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      Stein, Evan G.; Gustafson, Thomas A.; Hubbard, Stevan R. [Reprint author]
      Department of Pharmacology, Skirball Institute of Biomolecular Medicine,
CS
      New York University School of Medicine, 540 First Avenue, New York, NY,
      10016, USA
      hubbard@tallis.med.nyu.edu
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      Bereziat, V. [Reprint author]; Kasus-Jacobi, A. [Reprint author]; Perdereau, D. [Reprint author]; Girard, J. [Reprint author]; Burnol, A.-F.
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      [Reprint author]
      CNRS UPR1524, ICGM, 9 rue Jules Hetzel, 92190, Meudon, France
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Department of Biochemistry & Medical Genetics, University of Manitoba,
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Biochemistry and Cell Biology (2001), 79(1), 21-32
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      the endothelial cell-specific receptor tyrosine_kinase, Tek/Tie-2
ΑU
      Jones, Nina [Ph.D.]; Dumont, Daniel J. [adviser]
     University of Toronto (Canada) (0779)
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                      proteins for screening compounds capable of modulating
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     Burnol, Anne-Francoise; Perdereau, Dominique; Kasus-Jacobi, Anne;
     Bereziat, Veronique; Girard, Jean
     Centre National De La Recherche Scientifique-CNRS, Fr.
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     PCT Int. Appl., 46 pp.
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                ***Grb14*** . Characterization of a new receptor binding
     Reilly, John F.; Mickey, Gregory; Maher, Pamela A. [Reprint author]
Dept. of Cell Biology, The Scripps Research Institute, 10550 N. Torrey
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     Pines Rd., CAL-3, La Jolla, CA, 92037, USA
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     Kasus-Jacobi, Anne; Bereziat, Veronique; Perdereau, Dominique; Girard,
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     Endocrinologie Metabolisme et Developpement, CNRS, UPR 1524, 9 Rue Jules
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     Morrione, Andrea [Reprint author]
     Kimmel Cancer Center, Thomas Jefferson University, 233 South 10th Street,
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     Daly, Roger John; Sutherland, Robert Lyndsay
     Garvan Institute of Medical Research, Australia
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     Sunnybrook and Women's College Health Sciences Centre, 2075 Bayview Ave.,
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     Entered STN: 11 Oct 2000
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- DT Article
- English
- 0S Genbank-AF076619
- ED Entered STN: 18 Nov 1998 Last Updated on STN: 18 Nov 1998
- L2 ANSWER 76 OF 156 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN **DUPLICATE 41**
- 1998:251777 BIOSIS AN
- PREV199800251777 DN
- ΤI
- Interaction of the Grb10 adapter protein with the Raf1 and MEK1 kinases. Nantel, Andre [Reprint author]; Mohammad-Ali, Khosro; Sherk, Jennifer; ΑU
- Posner, Barry I.; Thomas, David Y. Eukaryotic Genet. Group, Biotechnol. Res. Inst., Natl. Res. Council, 6100 CS Royalmount, Montreal, PQ H4P 2R2, Canada
- Journal of Biological Chemistry, (April 24, 1998) Vol. 273, No. 17, pp. SO 10475-10484. print. CODEN: JBCHA3. ISSN: 0021-9258.
- Article
- LA English
- Entered STN: 9 Jun 1998 ED
 - Last Updated on STN: 12 Aug 1998
- L2 ANSWER 77 OF 156 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN **DUPLICATE 42**
- AN 1998:225785 BIOSIS
- PREV199800225785 DN
- TT Grb10 interacts differentially with the insulin receptor, insulin-like growth factor I receptor, and epidermal growth factor receptor via the Grb10 Src homology 2 (SH2) domain and a second novel domain located between the Pleckstrin homology and SH2 domains.
 He, Weimin; Rose, David W.; Olefsky, Jerrold M.; Gustafson, Thomas A.
- ΑU [Reprint author]
- 3876 Bay Cent. Pl., Hayward, CA 94545, USA CS Metabolex Inc.
- SO Journal of Biological Chemistry, (March 20, 1998) Vol. 273, No. 12, pp. 6860-6867. print. CODEN: JBCHA3. ISSN: 0021-9258.
- Article DT
- English LA
- ED Entered STN: 20 May 1998
- Last Updated on STN: 20 May 1998

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ΑN
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GΑ
                                          ***Grb14***
     A novel FGF signaling pathway u ***Grb14
Reilly J F (Reprint); Mickey G; Maher P A
                                                          binds to FGF receptor 1.
ΤI
ΑU
     SCRIPPS RES INST, DEPT CELL BIOL, LA JOLLA, CA 92037
CS
CYA
     USA
     MOLECULAR BIOLOGY OF THE CELL, (NOV 1998) Vol. 9, Supp. [S], pp.
SO
     1365-1365.
     Publisher: AMER SOC CELL BIOLOGY, PUBL OFFICE, 9650 ROCKVILLE PIKE,
     BETHESDA, MD 20814.
     ISSN: 1059-1524.
DT
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FS
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     English
LA
     Reference Count: 0
REC
     ANSWER 79 OF 156 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
L2
     1998:443196 BIOSIS
ΑN
DN
     PREV199800443196
     The Grb7 family of signalling proteins.
TI
     Daly, Roger J. [Reprint author]
ΑU
CS
     Cancer Res. Program, Garvan Inst. Med. Res., St. Vincent's Hosp., Sydney,
     NSW 2010, Australia
     Cellular Signalling, (Oct., 1998) Vol. 10, No. 9, pp. 613-618. print. CODEN: CESIEY. ISSN: 0898-6568.
SO
DT
     Article
     General Review; (Literature Review)
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     Entered STN: 21 Oct 1998
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     Last Updated on STN: 21 Oct 1998
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12
     1999:16001 BIOSIS
AN
     PREV199900016001
DN
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ΤI
     A novel FGF signaling pathway u
                                                          binds to FGF receptor 1.
     Reilly, John F.; Mickey, Gregory; Maher, Pamela A.
Dep. Cell Biol., Scripps Res. Inst., La Jolla, CA 92037, USA
CS
     Molecular Biology of the Cell, (Nov., 1998) Vol. 9, No. SUPPL., pp. 236A.
SO
     Meeting Info.: 38th Annual Meeting of the American Society for Cell
     Biology. San Francisco, California, USA. December 12-16, 1998. American
     Society for Cell Biology.
     CODEN: MBCEEV. ISSN: 1059-1524.
     Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
DT
     English
     Entered STN: 20 Jan 1999
ED
     Last Updated on STN: 20 Jan 1999
L2
     ANSWER 81 OF 156 DISSABS COPYRIGHT (C) 2004 ProQuest Information and
     Learning Company; All Rights Reserved on STN
     97:70470 DISSABS
                           Order Number: AAR0598267 (not available for sale by
     UMI)
TT
     ERBB RECEPTOR SIGNALLING IN HUMAN BREAST CANCER (TYROSINE KINASES)
     JANES, PETER WARWICK [PH.D.]
     UNIVERSITY OF NEW SOUTH WALES (AUSTRALIA) (0423)
     Dissertation Abstracts International, (1997) Vol. 58, No. 6B, p. 2970. Order No.: AARO598267 (not available for sale by UMI).
S0
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     DUPLICATE 43
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     Cloning, chromosome localization, expression, and characterization of an
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     Src homology 2 and pleckstrin homology domain-containing insulin receptor
     binding protein hGrb10gamma.
```

Dong, Lily Q.; Du, Hongyan; Porter, Sarah G.; Kolakowski, Lee F., Jr.;

Lee, Adrian V.; Mandarino, J.; Fan, Jianbing; Yee, Douglas; Liu, Feng

ΑU

[Reprint author]

```
CS
     Dep. Pharmacol., Univ. Texas Health Sci. Cent., 7703 Floyd Curl Dr., San
     Antonio, TX 78284-7764, USA
SO
     Journal of Biological Chemistry, (Nov. 14, 1997) Vol. 272, No. 46, pp.
     29104-29112. print.
     CODEN: JBCHA3. ISSN: 0021-9258.
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     1997:221295 BIOSIS
     PREV199799513011
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     Structural determinants of the interaction between the erbB2 receptor and
TΤ
     the Src homology 2 domain of Grb7.
     Janes, Peter W.; Lackmann, Martin; Church, W. Bret; Sanderson, Georgina
ΑU
     M.; Sutherland, Robert L.; Daly, Roger J. [Reprint author]
     Cancer Res. Program, Garvan Inst. Med. Res., St. Vincent's Hosp., Sydney,
CS
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     Journal of Biological Chemistry, (1997) Vol. 272, No. 13, pp. 8490-8497.
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     Last Updated on STN: 22 May 1997
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     1997:110178
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     PREV199799409381
DN
     Human GRB-IR-beta/GRB10: Splice variants of an insulin and growth factor
TI
     receptor-binding protein with PH and SH2 domains.
     Frantz, J. Daniel; Giorgetti-Peraldi, Sophie; Ottinger, Elizabeth A.;
ΑU
     Shoelson, Steven E. [Reprint author]
     Joslin Diabetes Cent., One Joslin Place, Boston, MA 02215, USA
Journal of Biological Chemistry, (1997) Vol. 272, No. 5, pp. 2659-2667.
CS
S0
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LA
     Entered STN: 10 Mar 1997
ED
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AN
     1997:26254 CAPLUS
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     126:43162
     GDU: a new target for the erbB family of protein tyrosine kinases and a
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     cDNA encoding it
IN
     Daly, Roger John; Sutherland, Robert Lyndsay
     Garvan Institute of Medical Research, Australia; Daly, Roger John;
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     Sutherland, Robert Lyndsay
SO
     PCT Int. Appl., 15 pp.
     CODEN: PIXXD2
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              SG, SI
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     Cloning and characterization of
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     GRB7 gene family.
     Daly, Roger J. [Reprint author]; Sanderson, Georgina M.; Janes, Peter W.;
ΑU
     Sutherland, Robert L.
     Cancer Biol. Div., Garvan Inst. Med. Res., St. Vincent's Hosp., Sydney,
     NSW 2010, Australia
Journal of Biological Chemistry, (1996) Vol. 271, No. 21, pp. 12502-12510.
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     Assignment of the human
     fluorescence in situ hybridization.
     Baker, Elizabeth; Sutherland, Grant R.; Sutherland, Robert L.; Daly, Roger
     J. [Reprint author]
     Cancer Biol. Div., Garvan Inst. Med. Res., St. Vincent's Hosp., Sydney,
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     Genomics, (1996) Vol. 36, No. 1, pp. 218-220.
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     CODEN: GNMCEP. ISSN: 0888-7543.
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     Article
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      Identification and selection of specific interaction agents by phage
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      display, comprises using a carrier with a polymer-free surface to which affinity ligands are bound.
      Hill O; Ottleben н
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      WO 2003102591 A2 20031211
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DATE (DATE):
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                         Lu, F.; Murphy, B.; Ferriera, S.; Wang, G.; Zheng, X.H.;
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                         Inferring nonneutral evolution from human-chimp-mouse
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   OTHER SOURCE (OS):
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White,T.J.; Sninsky,J.J.; Adams,M.D.; Cargill,M.
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Inferring nonneutral evolution from human-chimp-mouse
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science, 302 (5652), 1960-1963 (2003)
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   JOURNAL (SO):
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     ANSWER 95 OF 156
                                          COPYRIGHT 2004 on STN
                           GENBANK.RTM.
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LOCUS (LOC):
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GenBank VERSION (VER):
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                         17 Dec 2003
DATE (DATE):
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                         Hominidae; Homo
COMMENT:
     These sequences were made by sequencing genomic exons and ordering
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REFERENCE:
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   AUTHOR (AU):
                         Clark, A.G.; Glanowski, S.; Nielson, R.; Thomas, P.;
                         Kejariwal,A.; Todd,M.A.; Tanenbaum,D.M.; Civello,D.R.;
                         Lu,F.; Murphy,B.; Ferriera,S.; Wang,G.; Zheng,X.H.;
                         White, T.J.; Sninsky, J.J.; Adams, M.D.; Cargill, M. Inferring nonneutral evolution from human-chimp-mouse
   TITLE (TI):
                         orthologous gene trios
Science, 302 (5652), 1960-1963 (2003)
   JOURNAL (SO):
                         CA 140:140421
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REFERENCE:
   AUTHOR (AU):
                         Clark, A.G.; Glanowski, S.; Nielson, R.; Thomas, P.;
                         Kejariwal,A.; Todd,M.A.; Tanenbaum,D.M.; Civello,D.R.;
                         Lu,F.; Murphy,B.; Ferriera,S.; Wang,G.; Zheng,X.H.;
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                         Direct Submission
   TITLE (TI):
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L2
     ANSWER 96 OF 156
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LOCUS (LOC):
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DIVISION CODE (CI):
                         Primates
DATE (DATE)
                         30 Jun 2004
DEFINITION (DEF):
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                         mRNA (cDNA clone MGC:61485 IMAGE:6162863), complete
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KEYWORDS (ST):
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SOURCE:
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ORGANISM (ORGN):
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COMMENT:
     Contact: MGC help desk
     Email: cgapbs-r@mail.nih.gov
     Tissue Procurement: ATCC/DCTD/DTP
     CDNA Library Preparation: Life Technologies, Inc.
     CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
     DNA Sequencing by: National Institutes of Health Intramural
     Sequencing Center (NISC),
     Gaithersburg, Maryland;
     Web site: http://www.nisc.nih.gov/
     Contact: nisc_mgc@nhgri.nih.gov
     Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
     Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
     Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
     Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
     McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
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     Clone distribution: MGC clone distribution information can be found
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through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

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REFERENCE:
                                Strausberg, R.L.; Feingold, E.A.; Grouse, L.H.;
Derge, J.G.; Klausner, R.D.; Collins, F.S.; Wagner, L.;
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    AUTHOR (AU):
                                 Buetow, K.H.; Schaefer, C.F.; Bhat, N.K.; Hopkins, R.F.;
                                 Jordan,H.; Moore,T.; Max,S.I.; Wang,J.; Hsieh,F.;
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                                 Gibbs, R.A.; Fahey, J.; Helton, E.; Ketteman, M.; Madan, A.;
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                                 Blakesley, R.W.; Touchman, J.W.; Green, E.D.;
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    TITLE (TI):
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    JOURNAL (SO):
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    OTHER SOURCE (OS):
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                                 Strausberg, R.
    AUTHOR (AU):
                                 Direct Submission
    TITLE (TI):
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    JOURNAL (SO):
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                                Office, National Cancer Institute, 31 Center Drive,
                                 Room 11A03, Bethesda, MD 20892-2590, USA
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L2
       ANSWER 97 OF 156
                                     GENBANK.RTM.
                                                          COPYRIGHT 2004 on STN
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DATE (DATE):
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COMMENT:
       NEDO human cDNA sequencing project supported by Ministry of
       Economy, Trade and Industry of Japan; cDNA full insert sequencing:
       Research Association for Biotechnology; cDNA library construction:
       Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported
       by Japan Key Technology Center etc.).
REFERENCE:
    AUTHOR (AU):
                                  Isogai,T.; Ota,T.; Nishikawa,T.; Hayashi,K.; Otsuki,T.;
                                  Sugiyama, T.; Suzuki, Y.; Nagai, K.; Sugano, S.; Ishii, S.;
                                  Kawai-Hio,Y.; Saito,K.; Yamamoto,J.; Wakamatsu,A.;
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    TITLE (TI):
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    JOURNAL (SO):
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   AUTHOR (AU):
                           Isogai,T.; Otsuki,T.
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                           Direct Submission
                            Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu,
   JOURNAL (SO):
                            Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp,
                           Tel:81-438-52-3975, Fax:81-438-52-3986)
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L2
     ANSWER 98 OF 156
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LOCUS (LOC):
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                            16 Apr 2003
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SOURCE:
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COMMENT:
      Contact: MGC help desk
      Email: cgapbs-r@mail.nih.gov
     Tissue Procurement: Gilbert Smith, Ph.D.
      cDNA Library Preparation: Life Technologies, Inc.
      cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
     DNA Sequencing by: Baylor College of Medicine Human Genome
     Sequencing Center
     Center code: BCM-HGSC
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Web site: http://www.hgsc.bcm.tmc.edu/cdna/

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Contact: amg@bcm.tmc.edu
      Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
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      Clone distribution: MGC clone distribution information can be found
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      Series: IRAK Plate: 40 Row: g Column: 24. ENCE: 1 (bases 1 to 870)
REFERENCE:
   AUTHOR (AU):
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                                Hale,Ś.; Gárcia,A.M.; Gay,Ĺ.J.; Hulyk,S.W.;
Villalon,D.K.; Muzny,D.M.; Sodergren,E.J.; Lu,X.;
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Identification of a novel human tankyrase through its
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       Contact: Yoshihide Hayashizaki
       Laboratory for Genome Exploration Research Group, RIKEN Genomic
       Sciences Center(GSC), Yokohama Institute
       The Institute of Physical and Chemical Research (RIKEN)
       1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216
       Email: genome-res@gsc.riken.go.jp
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       Thermostabilization and thermoactivation of thermolabile enzymes by
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Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.
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        Automated filtration-based high-throughput plasmid preparation
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        Carninci, P. and Hayashizaki, Y.
        High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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        Please visit our web site (http://genome.rtc.riken.go.jp) for
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REFERENCE:
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SOURCE:
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COMMENT:
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     Laboratory for Genome Exploration Research Group, RIKEN Genomic
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Sciences Center(GSC), Yokohama Institute
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      1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
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      Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
      Thermostabilization and thermoactivation of thermolabile enzymes by
      trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
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                                 Arakawa, T.; Carninci, P.; Endo, T.; Fukuda, S.; Fukunishi, Y.; Hara, A.; Hayatsu, N.; Hirozane, T.;
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                                                        Genome Science Laboratory in
                                                        RIKEN. Division of Experimental
Animal Research in Riken
                                                        contributed to prepare mouse
                                                        tissues. 1st strand cDNA was primed with a primer [5'
                                                        GAGAGAGAGCGCCGCAACTCGAGTTTTTTTT
                                                        TTTTTTTVN 3'], cDNA was prepared
                                                        by using trehalose
                                                        thermo-activated reverse
                                                       transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer
                                                        adapter of sequence [5
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GAGAGAGATTCTCGAGTTAATTAAATTAATCC

CCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

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    301 attaaacctt att
L2
      ANSWER 102 OF 156
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                                                   COPYRIGHT 2004 on STN
LOCUS (LOC):
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GenBank VERSION (VER):
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DIVISION CODE (CI):
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DATE (DATE):
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DEFINITION (DEF):
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                               adapter rGrb14 ( ***Grb14*** ) mRNA, mRNA sequence.
SOURCE:
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Sciurognathi; Muridae; Murinae; Mus
NUCLEIC ACID COUNT (NA): 117 a
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COMMENT:
      Contact: Yoshihide Hayashizaki
      Laboratory for Genome Exploration Research Group, RIKEN Genomic
      Sciences Center(GSC), Yokohama Institute
      The Institute of Physical and Chemical Research (RIKEN)
      1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
      Fax: 81-45-503-9216
      Email: genome-res@gsc.riken.go.jp,
      URL:http://genome.gsc.riken.go.jp/
      Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
      Thermostabilization and thermoactivation of thermolabile enzymes by
      trehalose and its application for the synthesis of full length
      CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
       Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.
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       Carninci, P. and Hayashizaki, Y.
       High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
      19-44 (1999)
       Please visit our web site (http://genome.rtc.riken.go.jp) for
      further details.
REFERENCE:
                                  (bases 1 to 334)
   AUTHOR (AU):
                               Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.;
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Yamanaka,I., Yano,R.H; Yasunishi,A.; Yokota,T.;
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                               Hayashizaki, Y.
   TITLE (TI):
                               RIKEN Mouse ESTs (Konno, H., et al.)
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JOURNAL (SO): Unpublished (2000)

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Feature Key Location Qualifier

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/note="Site-1: SalI; Site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken

contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5]

GAGAGAGAGCGCCCGCAACTCGAGTTTTTTTT TTTTTTTVN 3'], cDNA was prepared

by using trehalose thermo-activated reverse

transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'

GAGAGAGAGTTCTCGAGTTAATTAAATTAATCC CCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I.'

SEQUENCE (SEQ):

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L2 ANSWER 103 OF 156 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB559080 GenBank (R)

GenBank ACC. NO. (GBN): BB559080

GenBank VERSION (VER): BB559080.1 GI:9645446

CAS REGISTRY NO. (RN): 284979-54-0

SEQUENCE LENGTH (SQL): 319

MOLECULE TYPE (CI): mRNA; linear DIVISION CODE (CI): Expressed sequence tag

DATE (DATE):

1 Aug 2000 DEFINITION (DEF):

BB559080 RIKEN full-length enriched, 2 days pregnant adult female ovary Mus musculus cDNA clone E330037E03 3' similar to AF076619 Rattus norvegicus molecular adapter rGrb14 (***Grb14***) mRNA, mRNA sequence.

house mouse.

ORGANISM (ORGN): Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Euteleostomi; Mammalia; Eutheria; Rodentia;

Sciurognathi; Muridae; Murinae; Mus

NUCLEIC ACID COUNT (NA): 108 a 62 c 62 g COMMENT:

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Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center(GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

```
Tel: 81-45-503-9222
Fax: 81-45-503-9216
      Email: genome-res@gsc.riken.go.jp,
      URL:http://genome.gsc.riken.go.jp/
      Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki
       ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
      Thermostabilization and thermoactivation of thermolabile enzymes by
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      cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
        Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.
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       ,Y. and Hayashizaki,Y.
       Automated filtration-based high-throughput plasmid preparation
      system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
      19-44 (1999)
        Please visit our web site (http://genome.rtc.riken.go.jp) for
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REFERENCE:
                                  (bases 1 to 319)
                               Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.; Arakawa,T.; Carninci,P.; Endo,T.; Fukuda,S.;
    AUTHOR (AU):
                               Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.;
Hori,F.; Ishii,Y.; Ishikawa,J.; Ishikawa,T.; Itoh,M.;
Izawa,M.; Kadota,K.; Kagawa,I.; Kai,C.; Kawai,J.;
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    TITLE (TI):
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                                                    Riken Genomic Sciences Center and
                                                    Genome Science Laboratory in
                                                    RIKEN. Division of Experimental
                                                    Animal Research in Riken
                                                    contributed to prepare mouse
                                                    tissues. 1st strand cDNA was
                                                    primed with a primer [5]
                                                    GAGAGAGAGCGGCCGCAACTCGAGTTTTTTT
                                                    TTTTTTTVN 3'], cDNA was prepared
                                                    by using trehalose
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                                                    transcriptase and subsequently
                                                    enriched for full-length by
                                                    cap-trapper. Second strand cDNA
                                                   was prepared with the primer
                                                    adapter of sequence [5
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      ANSWER 104 OF 156
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LOCUS (LOC):
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GenBank ACC. NO. (GBN): BB558470
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DIVISION CODE (CI):
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DATE (DATE):
                              1 Aug 2000
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DEFINITION (DEF):
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SOURCE:
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NUCLEIC ACID COUNT (NA): 74 a
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COMMENT:
      Contact: Yoshihide Hayashizaki
      Laboratory for Genome Exploration Research Group, RIKEN Genomic
      Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
      1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
      Tel: 81-45-503-9222
      Fax: 81-45-503-9216
      Email: genome-res@gsc.riken.go.jp,
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      Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki
       N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
      Thermostabilization and thermoactivation of thermolabile enzymes by
      trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
       Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.
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      system. Genome Res. 9 (5), 463-470 (1999)
       Carninci, P. and Hayashizaki, Y.
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      19-44 (1999)
       Please visit our web site (http://genome.rtc.riken.go.jp) for
      further details.
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                              Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.;
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   AUTHOR (AU):
                              Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.
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                                             RIKEN. Division of Experimental
                                             Animal Research in Riken
                                             contributed to prepare mouse
                                             tissues. 1st strand cDNA was
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                                             GAGAGAGAGCGCCCGCAACTCGAGTTTTTTTT
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                                             GAGAGAGATTCTCGAGTTAATTAAATTAATCC
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GenBank VERSION (VER):
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DEFINITION (DEF):
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                                          ) mRNA, mRNA sequence.
SOURCE:
                           house mouse.
 ORGANISM (ORGN):
                           Mus musculus
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Sciurognathi; Muridae; Murinae; Mus
NUCLEIC ACID COUNT (NA): 106 a
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COMMENT:
     Contact: Yoshihide Hayashizaki
     Laboratory for Genome Exploration Research Group, RIKEN Genomic
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Sciences Center(GSC), Yokohama Institute

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Tel: 81-45-503-9222 Fax: 81-45-503-9216

The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

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URL:http://genome.gsc.riken.go.jp/
      Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki
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Thermostabilization and thermoactivation of thermolabile enzymes by
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        Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.
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       Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
       19-44 (1999)
        Please visit our web site (http://genome.rtc.riken.go.jp) for
      further details.
REFERENCE:
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   AUTHOR (AU):
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                                RIKEN Mouse ESTs (Konno, H., et al.)
Unpublished (2000)
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                                                      RIKEN. Division of Experimental Animal Research in Riken
                                                      contributed to prepare mouse
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                                                      GAGAGAGAGCGCCGCAACTCGAGTTTTTTT
                                                      TTTTTTTVN 3'], cDNA was prepared
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                                                      thermo-activated reverse
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      ANSWER 106 OF 156
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DATE (DATE):
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DEFINITION (DEF):
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SOURCE:
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Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus
NUCLEIC ACID COUNT (NA): 87 a
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                                                  38 g
COMMENT:
      Contact: Yoshihide Hayashizaki
      Laboratory for Genome Exploration Research Group, RIKEN Genomic
      Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
      1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216
      Email: genome-res@gsc.riken.go.jp,
      URL:http://genome.gsc.riken.go.jp/
      Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
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      Thermostabilization and thermoactivation of thermolabile enzymes by
      trehalose and its application for the synthesis of full length
      CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
      Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
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        Automated filtration-based high-throughput plasmid preparation
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        Carninci, P. and Hayashizaki, Y.
        High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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        Please visit our web site (http://genome.rtc.riken.go.jp) for
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REFERENCE:
                               1 (bases 1 to 231)
                               Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.;
Arakawa,T.; Carninci,P.; Endo,T.; Fukuda,S.;
Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.;
Hori,F.; Ishii,Y.; Ishikawa,J.; Ishikawa,T.; Itoh,M.;
Izawa,M.; Kadota,K.; Kagawa,I.; Kai,C.; Kawai,J.;
    AUTHOR (AU):
                               Kikuchi, N.; Kiyosawa, H.; Kojima, Y.; Kondo, S.; Koya, S.;
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                                         GAGAGAGAGAGGATCCAAGAGCTCTTTTTTTT
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                                         round of normalization to Rot =
                                         10.0 and subtraction to Rot =
                                         185.0. Second strand cDNA was
                                         prepared with the primer adapter
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                                         GAGAGAGATTCTCGAGTTAATTAAATTAATCC
                                         CCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites.
                                         Vector: a modified pBluescript KS(+) after bulk excision from
                                         Lambda FLC I. Cloning sites, 5' end: Sall; 3' end: BamHI"
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  Laboratory for Genome Exploration Research Group, RIKEN Genomic
  Sciences Center(GSC), Yokohama Institute
  The Institute of Physical and Chemical Research (RIKEN)
  1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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SOURCE:

COMMENT:

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DEFINITION (DEF):

ORGANISM (ORGN):

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NUCLEIC ACID COUNT (NA): 103 a

Tel: 81-45-503-9222 Fax: 81-45-503-9216

Contact: Yoshihide Hayashizaki

Email: genome-res@gsc.riken.go.jp,

BB360354

284

279047-92-6

mRNA; linear

12 Jul 2000

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Mus musculus

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      Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki
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      Thermostabilization and thermoactivation of thermolabile enzymes by
      trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
       Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.
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       Carninci,P. and Hayashizaki,Y.
       High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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                                                  contributed to prepare mouse
                                                  tissues. 1st strand cDNA was
                                                  primed with a primer [5]
                                                  GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTT
                                                  TTTTTTTVN 3'], cDNA was prepared
                                                  by using trehalose
                                                  thermo-activated reverse
                                                  transcriptase and subsequently
                                                  enriched for full-length by
                                                  cap-trapper. cDNA went through one
                                                  round of normalization to Rot =
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into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5 end: SalI; 3' end: BamHI"

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SOURCE:
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NUCLEIC ACID COUNT (NA): 92 a
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COMMENT:
      Contact: Yoshihide Hayashizaki
      Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
      1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
      Tel: 81-45-503-9222
      Fax: 81-45-503-9216
      Email: genome-res@gsc.riken.go.jp,
      URL:http://genome.gsc.riken.go.jp/
      Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki
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      Thermostabilization and thermoactivation of thermolabile enzymes by
      trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
       Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.
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       Automated filtration-based high-throughput plasmid preparation
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       High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
      19-44 (1999)
       Please visit our web site (http://genome.rtc.riken.go.jp) for
      further details.
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REFERENCE:
   AUTHOR (AU):
                             Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.;
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RIKEN Mouse ESTs (Konno, H., et al.)

TITLE (TI):

JOURNAL (SO): Unpublished (2000)

FEATURES (FEAT):

Feature Key

Location

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Qualifier

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Contact: Yoshihide Hayashizaki
           Laboratory for Genome Exploration Research Group, RIKEN Genomic
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
           Tel: 81-45-503-9222
           Fax: 81-45-503-9216
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           Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
           Thermostabilization and thermoactivation of thermolabile enzymes by
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Animal Research in Riken
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                                                                                            tissues. 1st strand cDNA was
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NUCLEIC ACID COUNT (NA): 162 a
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COMMENT:
      Contact: Yoshihide Hayashizaki
      Laboratory for Genome Exploration Research Group, RIKEN Genomic
      Sciences Center(GSC), Yokohama Institute
      The Institute of Physical and Chemical Research (RIKEN)
      1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
      Fax: 81-45-503-9216
      Email: genome-res@gsc.riken.go.jp,
      URL:http://genome.gsc.riken.go.jp/
      Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
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      Thermostabilization and thermoactivation of thermolabile enzymes by
      trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
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       High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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       Please visit our web site (http://genome.rtc.riken.go.jp) for
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REFERENCE:
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                                              contributed to prepare mouse
                                              tissues. 1st strand cDNA was
                                              primed with a primer [5
                                              GAGAGAGAGAGGATCCAAGAGCTCTTTTTTTT
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                                              prepared with the primer adapter
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                                              Lambda FLC I. ~Retina RNA was
                                              provided by Stefano Gustincich,
                                              Department of Neurobiology
                                              Harvard Medical School, 220
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                                              gratefully acknowledge
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TITLE (TI):

FEATURES (FEAT):

Feature Key

SEQUENCE (SEQ):

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LOCUS (LOC):

source

JOURNAL (SO):

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NUCLEIC ACID COUNT (NA): 92 a
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COMMENT:
      Contact: Yoshihide Hayashizaki
      Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
      1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
      Fax: 81-45-503-9216
      Email: genome-res@gsc.riken.go.jp,
      URL:http://genome.gsc.riken.go.jp/
      Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki
       N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
      Thermostabilization and thermoactivation of thermolabile enzymes by
      trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
       Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.
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       Automated filtration-based high-throughput plasmid preparation
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       Carninci, P. and Hayashizaki, Y.
       High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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        Please visit our web site (http://genome.rtc.riken.go.jp) for
      further details.
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REFERENCE:
    AUTHOR (AU):
                              Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.;
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                                                   Genome Science Laboratory in
```

RIKEN. Division of Experimental

Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5 GAGAGAGAAGGATCCAAGAGCTCTTTTTTTT TTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5'GAGAGAGAGATTCTCGAGTTAATTAAATTAA TCCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. ~Retina RNA was provided by Stefano Gustincich, Department of Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA02115, USA, whose assistance we gratefully acknowledge

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COMMENT:
     Contact: Yoshihide Hayashizaki
     Laboratory for Genome Exploration Research Group, RIKEN Genomic
     Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
     1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
     Tel: 81-45-503-9222
     Fax: 81-45-503-9216
     Email: genome-res@gsc.riken.go.jp,
     URL:http://genome.gsc.riken.go.jp/
     Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
      Thermostabilization and thermoactivation of thermolabile enzymes by
     trehalose and its application for the synthesis of full length
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       Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.
      Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
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Carninci, P. and Hayashizaki, Y.
       High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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       Please visit our web site (http://genome.rtc.riken.go.jp) for
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                            Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.;
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                            Arakawa, T.; Carninci, P.; Endo, T.; Fukuda, S.;
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                                                tissues. 1st strand cDNA was
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SOURCE:
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COMMENT:
           Contact: Yoshihide Hayashizaki
           Laboratory for Genome Exploration Research Group, RIKEN Genomic
           Sciences Center(GSC), Yokohama Institute
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           1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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            Thermostabilization and thermoactivation of thermolabile enzymes by
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High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5 GAGAGAGAGAGGATCCAAGAGCTCTTTTTTTT TTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5 GAGAGAGATTCTCGAGTTAATTAAATTAATCC CCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. "

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                          30 Jun 2000
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DEFINITION (DEF):
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SOURCE:
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                          Sciurognathi; Muridae; Murinae; Mus
NUCLEIC ACID COUNT (NA): 87 a
                                   32 c
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COMMENT:
     Contact: Yoshihide Hayashizaki
     Laboratory for Genome Exploration Research Group, RIKEN Genomic
     Sciences Center(GSC), Yokohama Institute
     The Institute of Physical and Chemical Research (RIKEN)
     1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
     Tel: 81-45-503-9222
     Fax: 81-45-503-9216
     Email: genome-res@gsc.riken.go.jp,
     URL:http://genome.gsc.riken.go.jp/
     Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
     trehalose and its application for the synthesis of full length
     cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
      Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.
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      Automated filtration-based high-throughput plasmid preparation
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system. Genome Res. 9 (5), 463-470 (1999)

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Carninci, P. and Hayashizaki, Y.
       High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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        Please visit our web site (http://genome.rtc.riken.go.jp) for
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                                                     Genome Science Laboratory in
                                                     RIKEN. Division of Experimental
Animal Research in Riken
                                                     contributed to prepare mouse
                                                     tissues. 1st strand cDNA was
                                                     primed with a primer [5
                                                     GAGAGAGAGAGCTCTTTTTTTT
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                                                     by using trehalose
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                                                     transcriptase and subsequently enriched for full-length by
                                                     cap-trapper. cDNA went through one
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L2
      ANSWER 115 OF 156
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LOCUS (LOC): BB173204 GenBank (R)

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SOURCE:
 ORGANISM (ORGN):
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Sciurognathi; Muridae; Murinae; Mus
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NUCLEIC ACID COUNT (NA): 98 a
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COMMENT:
       Contact: Yoshihide Hayashizaki
       Laboratory for Genome Exploration Research Group, RIKEN Genomic
       Sciences Center(GSC), Yokohama Institute
       The Institute of Physical and Chemical Research (RIKEN)
       1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
       Tel: 81-45-503-9222
Fax: 81-45-503-9216
       Email: genome-res@gsc.riken.go.jp,
       URL:http://genome.gsc.riken.go.jp/
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       Thermostabilization and thermoactivation of thermolabile enzymes by
       trehalose and its application for the synthesis of full length
       CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.
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       ,Y. and Hayashizaki,Y.
        Automated filtration-based high-throughput plasmid preparation
       system. Genome Res. 9 (5), 463-470 (1999)
        Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
       19-44 (1999)
        Please visit our web site (http://genome.rtc.riken.go.jp) for
       further details.
REFERENCE:
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    AUTHOR (AU):
                                 Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.;
                                Arakawa,T.; Carninci,P.; Endo,T.; Fukuda,S.;
Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.;
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and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5 thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5 with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I.

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L2
     ANSWER 116 OF 156
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                                             COPYRIGHT 2004 on STN
LOCUS (LOC):
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GenBank VERSION (VER):
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DIVISION CODE (CI):
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DATE (DATE)
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                           rGrb14 (
                                                    ) mRNA, mRNA sequence.
SOURCE:
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Sciurognathi; Muridae; Murinae; Mus
NUCLEIC ACID COUNT (NA): 79 a
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COMMENT:
     Contact: Yoshihide Hayashizaki
     Laboratory for Genome Exploration Research Group, RIKEN Genomic
     Sciences Center(GSC), Yokohama Institute
     The Institute of Physical and Chemical Research (RIKEN)
     1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
     Fax: 81-45-503-9216
     Email: genome-res@gsc.riken.go.jp,
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     Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
     Thermostabilization and thermoactivation of thermolabile enzymes by
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     cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
      Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.
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      Automated filtration-based high-throughput plasmid preparation
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system. Genome Res. 9 (5), 463-470 (1999)

Carninci, P. and Hayashizaki, Y.

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High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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       Please visit our web site (http://genome.rtc.riken.go.jp) for
      further details.
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REFERENCE:
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                                                  Genome Science Laboratory in
                                                  RIKEN. Division of Experimental Animal Research in Riken
                                                  contributed to prepare mouse
                                                  tissues. 1st strand cDNA was primed with a primer [5'
                                                  GAGAGAGAAGGATCCAAGAGCTCTTTTTTTT
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LOCUS (LOC):

BB124451

GenBank (R)

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COMMENT:
      Contact: Yoshihide Hayashizaki
      Laboratory for Genome Exploration Research Group, RIKEN Genomic
      Sciences Center(GSC), Yokohama Institute
      The Institute of Physical and Chemical Research (RIKEN)
      1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
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      Thermostabilization and thermoactivation of thermolabile enzymes by
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Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki Y. and Havashizaki Y.
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        High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
       19-44 (1999)
        Please visit our web site (http://genome.rtc.riken.go.jp) for
       further details.
                                   (bases 1 to 312)
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    AUTHOR (AU):
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LOCUS (LOC):
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SOURCE:
                            house mouse.
 ORGANISM (ORGN):
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                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus
NUCLEIC ACID COUNT (NA): 89 a
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                                      39 c
COMMENT:
      Contact: Yoshihide Hayashizaki
      Laboratory for Genome Exploration Research Group, RIKEN Genomic
      Sciences Center(GSC), Yokohama Institute
      The Institute of Physical and Chemical Research (RIKEN)
      1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
     Tel: 81-45-503-9222
Fax: 81-45-503-9216
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      Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
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       Automated filtration-based high-throughput plasmid preparation
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system. Genome Res. 9 (5), 463-470 (1999)
       Carninci, P. and Hayashizaki, Y.
       High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
      19-44 (1999)
       Please visit our web site (http://genome.rtc.riken.go.jp) for
      further details.
REFERENCE:
                             1 (bases 1 to 235)
   AUTHOR (AU):
                             Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.;
                             Arakawa, T.; Carninci, P.; Endo, T.; Fukuda, S.; Fukunishi, Y.; Hara, A.; Hayatsu, N.; Hirozane, T.;
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Mizuno,Y.; Nakamura,M.; Oda,H.; Okazaki,Y., Ono,T.y;
Owa,C.; Saito,H.; Sakai,C.; Sato,K.; Shibata,K.;
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                                                Genome Science Laboratory in
                                                RIKEN. Division of Experimental Animal Research in Riken
                                                contributed to prepare mouse
                                                tissues. 1st strand cDNA was
                                                primed with a primer [5
                                                GAGAGAGAGAGGATCCAAGAGCTCTTTTTTTT
                                                TTTTTTTVN 3'], cDNA was prepared
                                                by using trehalose
                                                thermo-activated reverse
                                                transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one
                                                round of normalization to Rot =
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                                                of sequence [5
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DATE (DATE):
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DEFINITION (DEF):
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NUCLEIC ACID COUNT (NA): 110 a
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COMMENT:
       Contact: Yoshihide Hayashizaki
       Laboratory for Genome Exploration Research Group, RIKEN Genomic
       Sciences Center(GSC), Yokohama Institute
       The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
       Tel: 81-45-503-9222
       Fax: 81-45-503-9216
       Email: genome-res@gsc.riken.go.jp,
       URL:http://genome.gsc.riken.go.jp/
       Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki
       N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
       Thermostabilization and thermoactivation of thermolabile enzymes by
       trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
       ,Y. and Hayashizaki,Y.
        Automated filtration-based high-throughput plasmid preparation
       system. Genome Res. 9 (5), 463-470 (1999)
        Carninci,P. and Hayashizaki,Y.
        High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
       19 - \overline{44} (1999)
         Please visit our web site (http://genome.rtc.riken.go.jp) for
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REFERENCE:
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    AUTHOR (AU):
                                  Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.;
                                 Arakawa,T.; Carninci,P.; Endo,T.; Fukuda,S.; Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.; Hori,F.; Ishii,Y.; Ishikawa,J.; Ishikawa,T.; Itoh,M.; Izawa,K.; Kadota,K.; Kagawa,I.; Kai,C.; Kawai,J.;
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L2
      ANSWER 120 OF 156
                              GENBANK.RTM.
                                               COPYRIGHT 2004 on STN
LOCUS (LOC):
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GenBank VERSION (VER):
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SEQUENCE LENGTH (SQL):
MOLECULE TYPE (CI):
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DIVISION CODE (CI):
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DATE (DATE):
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DEFINITION (DEF):
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SOURCE:
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Sciurognathi; Muridae; Murinae; Mus
NUCLEIC ACID COUNT (NA): 102 a
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COMMENT:
      Contact: Yoshihide Hayashizaki
      Laboratory for Genome Exploration Research Group, RIKEN Genomic
      Sciences Center(GSC), Yokohama Institute
      The Institute of Physical and Chemical Research (RIKEN)
      1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
      Fax: 81-45-503-9216
      Email: genome-res@gsc.riken.go.jp,
      URL:http://genome.gsc.riken.go.jp/
      Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki
      ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
      Thermostabilization and thermoactivation of thermolabile enzymes by
      trehalose and its application for the synthesis of full length
      CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
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Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki

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,Y. and Hayashizaki,Y.
       Automated filtration-based high-throughput plasmid preparation
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      19-44 (1999)
       Please visit our web site (http://genome.rtc.riken.go.jp) for
      further details.
REFERENCE:
                              1 (bases 1 to 249)
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                              Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.;
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Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.;
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                                                  Genome Science Laboratory in
                                                  RIKEN. Division of Experimental
                                                  Animal Research in Riken
                                                  contributed to prepare mouse
                                                  tissues. 1st strand cDNA was
                                                  primed with a primer [5
                                                  GAGAGAGAAGGATCCAAGAGCTCTTTTTTTT
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                                                  by using trehalose
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L2
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SOURCE:
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NUCLEIC ACID COUNT (NA): 93 a
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COMMENT:
           Contact: Yoshihide Hayashizaki
           Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
           The Institute of Physical and Chemical Research (RIKEN)
           1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
           Tel: 81-45-503-9222
           Fax: 81-45-503-9216
           Email: genome-res@gsc.riken.go.jp,
           URL:http://genome.gsc.riken.go.jp/
          Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, R., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, J., Tomaru, Y., Carninci, R., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, J., Tomaru, Y., Carninci, R., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, J., Tomaru, Y., Carninci, R., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, J., Okazaki, Y., Okazaki,
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             Carninci, P. and Hayashizaki, Y.
             High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
           19-44 (1999)
             Please visit our web site (http://genome.rtc.riken.go.jp) for
           further details.
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      AUTHOR (AU):
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                                        Animal Research in Riken
                                        contributed to prepare mouse
                                        tissues. 1st strand cDNA was
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                                        Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI"
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 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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DATE (DATE):

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COMMENT:

ANSWER 122 OF 156

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GenBank VERSION (VER):

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DIVISION CODE (CI):

DEFINITION (DEF):

ORGANISM (ORGN):

NUCLEIC ACID COUNT (NA): 113 a

Tel: 81-45-503-9222 Fax: 81-45-503-9216

Contact: Yoshihide Hayashizaki

Email: genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/

BB045416

BB045416

323

BB045416.1

272392-50-4

mRNA; linear

23 Jun 2000

house mouse.

Mus musculus

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63 c

Thermostabilization and thermoactivation of thermolabile enzymes by

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trehalose and its application for the synthesis of full length
      cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
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        Carninci, P. and Hayashizaki, Y.
        High-efficiency full-length cDNA cloning. Methods Enzymol. 303.
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                                                         Genome Science Laboratory in
                                                         RIKEN. Division of Experimental
                                                         Animal Research in Riken
                                                         contributed to prepare mouse
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                                                         primed with a primer [5'
                                                         GAGAGAGAAGGATCCAAGAGCTCTTTTTTTT
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                                                         prepared with the primer adapter
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Lambda FLC I. Cloning sites, 5

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NUCLEIC ACID COUNT (NA): 104 a
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COMMENT:
      Contact: Yoshihide Hayashizaki
      Laboratory for Genome Exploration Research Group, RIKEN Genomic
      Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
      1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
      Tel: 81-45-503-9222
      Fax: 81-45-503-9216
      Email: genome-res@gsc.riken.go.jp,
      URL:http://genome.gsc.riken.go.jp/
      Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
      N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
      Thermostabilization and thermoactivation of thermolabile enzymes by
      trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
       Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.
      Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
      ,Y. and Hayashizaki,Y.
       Automated filtration-based high-throughput plasmid preparation
      system. Genome Res. 9 (5), 463-470 (1999)
       Carninci, P. and Hayashizaki, Y.
       High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
       Please visit our web site (http://genome.rtc.riken.go.jp) for
      further details.
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                                (bases 1 to 289)
   AUTHOR (AU):
                             Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.;
                             Arakawa,T.; Carninci,P. ; Endo,T.; Fukuda,S.;
                             Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.
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   TITLE (TI):
                             Unpublished (2000)
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FEATURES (FEAT):
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Qualifier Location

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of sequence [5' GAGAGAGATTCTCGAGTTAATTAAATTAATCC CCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5 end: SalI; 3' end: BamHI." SEQUENCE (SEQ): 1 tctaccacta cacacggggt ctttcccccc aaccagcagc attactgtcc taggatcccc 61 gtttacccta actctgtgtc actcgttaca ccacagaaga agaaggatcc aaaggagaat 121 gattagagag agagagaga atcacaaggc tgaatacaaa tcatggtgaa aagaagattt 181 cacctgcggg ttacaaaaaa aaaataggtc acacattgca aattagtgaa aacttggatt 241 cctattacac tcatgacttt aaatttatta gttaaaatta aaccttatt L2 ANSWER 124 OF 156 GENBANK.RTM. COPYRIGHT 2004 on STN LOCUS (LOC): BB037605 GenBank (R) GenBank ACC. NO. (GBN): BB037605 GenBank VERSION (VER): BB037605.1 GI:8443991 CAS REGISTRY NO. (RN): 272314-39-3 SEQUENCE LENGTH (SQL): 237 MOLECULE TYPE (CI): mRNA; linear DIVISION CODE (CI): Expressed sequence tag DATE (DATE): 23 Jun 2000 BB037605 RIKEN full-length enriched, 13 days embryo forelimb Mus musculus cDNA clone 5930428012 3' similar DEFINITION (DEF): to AF076619 Rattus norvegicus molecular adapter rGrb14 ***Grb14***) mRNA, mRNA sequence. SOURCE: house mouse. ORGANISM (ORGN): Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus NUCLEIC ACID COUNT (NA): 84 a 50 c 40 g **COMMENT:** Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center(GSC), Yokohama Institute

```
The Institute of Physical and Chemical Research (RIKEN)
       1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
       Tel: 81-45-503-9222
       Fax: 81-45-503-9216
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       Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki
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       Thermostabilization and thermoactivation of thermolabile enzymes by
      trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
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        Automated filtration-based high-throughput plasmid preparation
       system. Genome Res. 9 (5), 463-470 (1999)
        Carninci, P. and Hayashizaki, Y.
        High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
       19-44 (1999)
        Please visit our web site (http://genome.rtc.riken.go.jp) for
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REFERENCE:
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                                                        Genome Science Laboratory in
                                                       RIKEN. Division of Experimental
                                                       Animal Research in Riken
                                                        contributed to prepare mouse
                                                        tissues. 1st strand cDNA was
                                                        primed with a primer [5
                                                        GAGAGAGAGAGGATCCAAGAGCTCTTTTTTTT
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                                                       by using trehalose
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                                                       transcriptase and subsequently
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100.0. Second strand cDNA was

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prepared with the primer adapter
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Association of fibroblast growth factor receptor 1 with
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                           J. Biol. Chem., 275 (11), 7771-7778 (2000)
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                           Reilly, J.F.; Mickey, G.; Maher, P.A.
                           Direct Submission
                           Submitted (01-JUN-1999) Cell Biology, The Scripps
Research Institute, 10550 N. Torrey Pines Rd., CAL-3,
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SOURCE:

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source

5'UTR

gene ČDS

ANSWER 125 OF 156

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AUTHOR (AU): TITLE (TI):

JOURNAL (SO):

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JOURNAL (SO):

TITLE (TI):

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Location

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mRNA; linear

19 Mar 2000

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Mus musculus

3'UTR

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L2 ANSWER 126 OF 156 GENBANK.RTM. COPYRIGHT 2004 on STN

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                                    ***Grb14*** ) mRNA, mRNA sequence.
SOURCE:
                          house mouse.
 ORGANISM (ORGN):
                          Mus musculus
                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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COMMENT:
     Contact: Yoshihide Hayashizaki
     Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
     The Institute of Physical and Chemical Research (RIKEN)
     1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
     Tel: 81-45-503-9222
     Fax: 81-45-503-9216
     Email: genome-res@gsc.riken.go.jp,
     URL:http://genome.gsc.riken.go.jp/
     Sasaki, N., Izawa, M., Watahiki, M., Ozawa, K., Tanaka, T., Yoneda, Y.
     Matsuura, S., Carninci, P., Muramatsu, M., Okazaki, Y. and Hayashizaki
      Transcriptional sequencing: A method for DNA sequencing using RNA
```

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polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
       Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.
      Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
       Automated filtration-based high-throughput plasmid preparation
      system. Genome Res. 9 (5), 463-470 (1999)
       Carninci, P. and Hayashizaki, Y.
       High-efficiency full-length cDNA cloning. Methods Enzymol. 303.
      19-44 (1999)
       Please visit our web site (http://genome.rtc.riken.go.jp) for
      further details.
REFERENCE:
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                             Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.;
Carninci,P.; Endo,T.; Fukuda,S.; Fukunishi,Y.; Hara,A.;
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                             Ishikawa,T.; Itoh,M.; Izawa,M.; Kadota,K.; Kagawa,I.;
Kai,C.?; Kawai,J.; Kikuchi,N.; Kojima,Y.; Koya,S.;
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      ANSWER 127 OF 156
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NUCLEIC ACID COUNT (NA): 93 a
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COMMENT:
      Contact: Yoshihide Hayashizaki
      Laboratory for Genome Exploration Research Group, RIKEN Genomic
      Sciences Center(GSC), Yokohama Institute
      The Institute of Physical and Chemical Research (RIKEN)
      1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
      Tel: 81-45-503-9222
      Fax: 81-45-503-9216
      Email: genome-res@gsc.riken.go.jp,
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      Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y., Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
       Transcriptional sequencing: A method for DNA sequencing using RNA
      polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
       Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
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       Automated filtration-based high-throughput plasmid preparation
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       Carninci, P. and Hayashizaki, Y.
       High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
      19-44 (1999)
       Please visit our web site (http://genome.rtc.riken.go.jp) for
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REFERENCE:
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                            Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.;
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 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.
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DATE (DATE):

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NUCLEIC ACID COUNT (NA): 73 a

Tel: 81-45-503-9222 Fax: 81-45-503-9216

Contact: Yoshihide Hayashizaki

Email: genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/

AV335961

193

AV335961.1

248628-93-5

mRNA; linear

11 Nov 1999

house mouse.

Mus musculus

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Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)

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Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
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       Please visit our web site (http://genome.rtc.riken.go.jp) for
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      Contact: Yoshihide Hayashizaki
      Laboratory for Genome Exploration Research Group, RIKEN Genomic
      Sciences Center(GSC), Yokohama Institute
      The Institute of Physical and Chemical Research (RIKEN)
      1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
      Tel: 81-45-503-9222
      Fax: 81-45-503-9216
      Email: genome-res@gsc.riken.go.jp,
      URL:http://genome.gsc.riken.go.jp/
      Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y., Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
       Transcriptional sequencing: A method for DNA sequencing using RNA
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       Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.
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       Automated filtration-based high-throughput plasmid preparation
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High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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       Please visit our web site (http://genome.rtc.riken.go.jp) for
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 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
  1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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 Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
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Tel: 81-45-503-9222 Fax: 81-45-503-9216

Contact: Yoshihide Hayashizaki

AV321727

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mRNA: linear

9 Nov 1999

house mouse.

Mus musculus

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Transcriptional sequencing: A method for DNA sequencing using RNA

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polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
       Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.
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                                                  and sequenced in Mouse Genome
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                                                  Exploration Research Group in
                                                  Riken Genomic Sciences Center and
                                                  Genome Science Laboratory in
                                                  RIKEN. Division of Experimental
                                                  Animal Research in Riken
                                                  contributed to prepare mouse
                                                  tissues. 1st strand cDNA was
                                                  primed with a primer [5
                                                  GAGAGAGAAGGATCCAAGAGCTCTTTTTTTT
                                                  TTTTTTTVN 3'], cDNA was prepared
                                                  by using trehalose
                                                  thermo-activated reverse
                                                  transcriptase and subsequently enriched for full-length by
                                                  cap-trapper. cDNA went through one
                                                  round of normalization to Rot =
                                                  5.0 and subtraction to Rot =
                                                  100.0. Second strand cDNA was
                                                  prepared with the primer adapter
of sequence [5'
                                                  GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC
CCCCCCCCC 3']. cDNA was cloned
into the XhoI and BamHI sites.
                                                  Vector: a modified pBluescript
                                                  KS(+) after bulk excision from
                                                  Lambda FLC I. Cloning sites, 5'
                                                  end: SalI; 3' end: BamHI.
```

¹ gcagccttac tgtgatcggc ttcctctttc cccaaactct cttttactcc tttatctaca

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61 gtagaagcag gttgcaagcg agaatgatta gagagtgaga gtgagattac caggctgata
121 acaattcatg gtgaaaagaa gatttcacct gcgggttaca aaaaaaaata ggtcacacat
     181 tgcaaattag tgaaaacttg gattcctatt acattcatga ctttaaattt attagttaaa
     241 attaaacctt att
       ANSWER 131 OF 156
                                     GENBANK.RTM.
                                                        COPYRIGHT 2004 on STN
LOCUS (LOC):
                                  AV259119
                                                    GenBank (R)
GenBank ACC. NO. (GBN): AV259119
GenBank VERSION (VER): AV259119
                                  AV259119.1 GI:6246578
CAS REGISTRY NO. (RN):
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SEQUENCE LENGTH (SQL):
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MOLECULE TYPE (CI):
DIVISION CODE (CI):
                                  mRNA; linear
                                  Expressed sequence tag
DATE (DATE):
                                  4 Nov 1999
DEFINITION (DEF):
                                  AV259119 RIKEN full-length enriched, adult male testis
                                  (DH10B) Mus musculus cDNA clone 4930403H14 3' similar
                                  to AF076619 Rattus norvegicus molecular adapter rGrb14
                                      ***Grb14*** ) mRNA, mRNA sequence.
SOURCE:
                                  house mouse.
 ORGANISM (ORGN):
                                  Mus musculus
                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                  Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus
NUCLEIC ACID COUNT (NA): 103 a
                                             27 c
                                                        34 g
COMMENT:
       Contact: Yoshihide Hayashizaki
       Laboratory for Genome Exploration Research Group, RIKEN Genomic
       Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
       1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
Fax: 81-45-503-9216
       Email: genome-res@gsc.riken.go.jp,
       URL:http://genome.gsc.riken.go.jp/
       Sasaki, N., Izawa, M., Watahiki, M., Ozawa, K., Tanaka, T., Yoneda, Y.
       Matsuura, S., Carninci, P., Muramatsu, M., Okazaki, Y. and Hayashizaki
        Transcriptional sequencing: A method for DNA sequencing using RNA
       polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
        Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
       Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
       ,Y. and Hayashizaki,Y.
        Automated filtration-based high-throughput plasmid preparation
       system. Genome Res. 9 (5), 463-470 (1999)
        Carninci,P. and Hayashizaki,Y.
        High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
       19-44 (1999)
        Please visit our web site (http://genome.rtc.riken.go.jp) for
       further details.
REFERENCE:
                                  1 (bases 1 to 230)
                                 Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.; Carninci, P.; Endo, T.; Fukuda, S.; Fukunishi, Y.; Hara, A.; Hayatsu, N.; Hirozane, T.; Hori, F.; Ishii, Y.; Ishikawa, T.; Itoh, M.; Izawa, M.; Kadota, K.; Kagawa, I.; Kai, C.?; Kawai, J.; Kikuchi, N.; Kojima, Y.; Koya, S.; Kusakabe, M.; Matsuyama, T.; Miki, R.; Mizuno, Y.; Nakamura, M.; Oda, H.; Okazaki, Y.; Owa, C.; Ozawa, Y.; Saito, H.; Sano, M.; Sato, K.; Shibata, K.; Shibata, Y.; Shigamoto, Y.; Shiraki, T.; Sogaba, Y.; Sugabara, Y.;
    AUTHOR (AU):
                                 Shigemoto, Y.; Shiraki, T.; Sogabe, Y.; Sugahara, Y.; Suzuki, H.; Suzuki, H.; Takahashi, F.; Tateno, M.; Tominaga, N.; Tsunoda, Y.; Watahiki, A.; Watanabe, S.; Yamamura, T.; Yasunishi, A.; Yokota, T.; Yoshiki, A.; Yoshino, M.; Muramatsu, M.; Hayashizaki, Y. RIKEN Mouse (STS (Konno, H., et al. 1999)
    TITLE (TI):
    JOURNAL (SO):
                                 Unpublished (1999)
FEATURES (FEAT):
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                            Location
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enriched, adult male testis

L2

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(DH10B)"
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                                          /dev-stage="adult
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                                          /note="Site-1: SalI; Site-2:
                                          BamHI; cDNA library was prepared
                                          and sequenced in Mouse Genome
                                          Encyclopedia Project of Genome
                                          Exploration Research Group in
                                          Riken Genomic Sciences Center and
                                          Genome Science Laboratory in
                                          RIKEN. Division of Experimental
                                          Animal Research in Riken
                                          contributed to prepare mouse
                                          tissues. 1st strand cDNA was
                                          primed with a primer [5'
                                          GAGAGAGAGAGGATCCAAGAGCTCTTTTTTTT
                                          TTTTTTVN 3'], cDNA was prepared
                                          by using trehalose
                                          thermo-activated reverse
                                         transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'
                                          GAGAGAGATTCTCGAGTTAATTAAATTAATCC
                                          CCCCCCCCC 3']. cDNA was cloned
                                          into the XhoI and BamHI sites.
                                          Vector: a modified pBluescript
                                          KS(+) after bulk excision from
                                          Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."
  1 atgttcttat ctaaacttct taatttaata cactaaagaa gaagaatgaa acaaagaaga
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121 ttaacctgcg ggttacaaaa aaaaatagtt cacacattgc aaattagtga aaacttggat
181 tectattaca atcatgaett taaatttatt agttaaaatt aaacettatt
                          GENBANK.RTM. COPYRIGHT 2004 on STN
                                      GenBank (R)
                                    GI:6018121
                       Rattus norvegicus growth factor receptor binding
                       protein GRB7 (Grb7) mRNA, complete cds.
                       Norway rat.
Rattus norvegicus
                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                       Euteleostomi; Mammalia; Eutheria; Rodentia;
                       Sciurognathi; Muridae; Murinae; Rattus
                                          548 g
                                                    462 t
                           (bases 1 to 2052)
                       Kasus-Jacobi,A.; Perdereau,D.; Auzan,C.; Clauser,E.;
                       Van Obberghen,E.; Mauvais-Jarvis,F.; Girard,J.;
                       Burnol,A.F.
Identification of the rat adapter
                                                                ***Grb14***
                                                                                as an
                       inhibitor of insulin actions
J. Biol. Chem., 273 (40), 26026-26035 (1998)
                           (bases 1 to 2052)
                       Kasus-Jacobi,A.; Bereziat,V.; Perdereau,D.; Girard,J.;
                       Evidence for an interaction between the insulin
                       receptor and Grb7. A role for two of its binding
                       domains, PIR and SH2
Oncogene, 19 (16), 2052-2059 (2000)
                           (bases 1 to 2052)
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SEQUENCE (SEQ):

LOCUS (LOC):

DATE (DATE):

SOURCE:

REFERENCE:

REFERENCE:

REFERENCE:

ANSWER 132 OF 156

GenBank VERSION (VER):

CAS REGISTRY NO. (RN):

SEQUENCE LENGTH (SQL):

MOLECULE TYPE (CI):

DIVISION CODE (CI):

DEFINITION (DEF):

ORGANISM (ORGN):

AUTHOR (AU):

TITLE (TI):

JOURNAL (SO): OTHER SOURCE (OS):

AUTHOR (AU):

TITLE (TI):

JOURNAL (SO): OTHER SOURCE (OS):

AUTHOR (AU):

GenBank ACC. NO. (GBN): AF190121

NUCLEIC ACID COUNT (NA): 440 a

AF190121

2052

Rodents

AF190121.1

244113-77-7

mRNA; linear

22 Nov 2000

CA 130:20710

Burnol,A.F.

CA 133:69252

602 c

Burnol, A.F.; Perdereau, D.; Kasus-Jacobi, A.

L2

TITLE (TI): JOURNAL (SO): Direct Submission

Submitted (27-SEP-1999) UPR 1524, CNRS, 9 rue Jules

QGLVDGVFLVRESQRNPQGFVLSLCHLQKVKHYL

ILPSEDEGCLYFSMDDGQTRFTDL LQLVEFHQLNRGILPCLLRHCCARVAL"

Hetzel, Meudon 92190, France

FEATURES (FEAT):

Feature Key Location Qualifier ____________ 1..2052 /organism="Rattus norvegicus" source /db-xref="taxon:10116" /tissue-type="liver"
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SEQUENCE (SEQ):

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LOCUS (LOC):
                          AI928176
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GenBank ACC. NO. (GBN): AI928176
GenBank VERSION (VER):
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SEQUENCE LENGTH (SQL):
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MOLECULE TYPE (CI):
                          mRNA; linear
DIVISION CODE (CI):
                          Expressed sequence tag
DATE (DATE):
                          8 Mar 2000
DEFINITION (DEF):
                          wo95a09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone
                          IMAGE:2463064 3' similar to TR:Q14449 Q14449
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                                         . ;, mRNA sequence.
SOURCE:
 ORGANISM (ORGN):
                          Homo sapiens
                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                          Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                          Hominidae; Homo
NUCLEIC ACID COUNT (NA): 90 a
                                  54 c
                                          48 q
                                                  127 t
COMMENT:
     Contact: Robert Strausberg, Ph.D.
     Email: cgapbs-r@mail.nih.gov
     Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
     Emmert-Buck, M.D., Ph.D.
      cDNA Library Preparation: M. Bento Soares, Ph.D.
      cDNA Library Arrayed by: Greg Lennon, Ph.D.
      DNA Sequencing by: Washington University Genome Sequencing Center
      Clone distribution: NCI-CGAP clone distribution information can be
     found through the I.M.A.G.E. Consortium/LLNL at:
     www-bio.lln1.gov/bbrp/image/image.html
     Insert Length: 399
                           Std Error: 0.00
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REFERENCE:
                          1 (bases 1 to 319)
   AUTHOR (AU):
                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                          National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
   TITLE (TI):
                          Unpublished (1997)
   JOURNAL (SO):
FEATURES (FEAT):
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                     Location
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                                           circles were made in vitro.
                                           Following HAP purification, this
                                           DNA was used as tracer in a
                                           subtractive hybridization
                                           reaction. The driver was PCR-amplified cDNAs from a pool of
                                           5,000 clones made from the same
                                           library (cloneIDs 1322376-1323911, 1456007-1456775, and
                                           1500552-1502855). Subtraction by
                                           Bento Soares and M. Fatima
                                           Bonaldo.
SEQUENCE (SEQ):
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   121 ttcacatgat aaigttticg cccttattta tggtctttta tiatiitict tgagtccttt
   181 teetteaata gittaataag teaetietgg etigietaga gageaateet ageacaataa
   241 tgtttcaact tgcaaggaag aacgccctta ttgagttgat agaactccac cagctgtatt
   301 agatctgtaa atcttgtgt
L2
     ANSWER 134 OF 156
                            GENBANK, RTM. COPYRIGHT 2004 on STN
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LOCUS (LOC): AI870172 GenBank (R) GenBank ACC. NO. (GBN): AI870172

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GenBank VERSION (VER):
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                                                                      5 others
 COMMENT:
      Contact: Robert Strausberg, Ph.D.
       Email: cgapbs-r@mail.nih.gov
       Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
      Emmert-Buck, M.D., Ph.D.
        CDNA Library Preparation: Life Technologies, Inc.
        CDNA Library Arrayed by: Greg Lennon, Ph.D.
        DNA Sequencing by: Washington University Genome Sequencing Center
        Clone distribution: NCI-CGAP clone distribution information can be
       found through the I.M.A.G.E. Consortium/LLNL at:
      www-bio.llnl.gov/bbrp/image/image.html
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      High quality sequence stop: 414.
REFERENCE:
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    AUTHOR (AU):
                             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
    TITLE (TI):
                             National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
    JOURNAL (SO):
                             Unpublished (1997)
FEATURES (FEAT):
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                                                 /lab-host="DH10B"
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                                                 catalog #: 11538-014
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   301 ttagatctgt aaatcttgtg tggccatcat ccagtgtgtg gaacatttca ccgtcatctt 361 ctactggtat aatttgaaag tgctttattt tttgtccatg actcattgac agtacgaaag 421 ttttggggtt actctgacta tcccgtacca agaaaactcc atccacaagt ccttgctgaa
    481 taatcaatcg ctgagcctca tctctagaaa tnttgtggtg aaaccatggc tgggaccggt
   541 ggatagccat gtntgtggca gagctctgtg aagagcagtg gggctaccgt gagtgcccag
601 gcgtaaacat cctttttnc tccaagcgag tccctcttca accgcaactg aaaggggctt
    661 ccgtgggatn ttctaatact ctgctťtťcc tgccctgaga agtčattgcť accagggaaa
    721 tctctgtnta cctcctcata ggtga
L2
      ANSWER 135 OF 156
                               GENBANK.RTM. COPYRIGHT 2004 on STN
LOCUS (LOC):
                             AI767914
                                             GenBank (R)
GenBank ACC. No. (GBN): AI767914
GenBank VERSION (VER):
                             AI767914.1 GI:5234435
CAS REGISTRY NO. (RN):
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SEQUENCE LENGTH (SQL):
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DIVISION CODE (CI):
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DATE (DATE):
                           21 Dec 1999
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***GRB14*** ; mRNA sequence
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                           Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                           Hominidae; Homo
: 112 a 74 c
NUCLEIC ACID COUNT (NA): 112 a
                                            74 g
                                                    168 t
                                                             1 others
COMMENT:
      Contact: Robert Strausberg, Ph.D.
      Email: cgapbs-r@mail.nih.gov
      Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
      Emmert-Buck, M.D., Ph.D.
       CDNA Library Preparation: M. Bento Soares, Ph.D.
       cDNA Library Arrayed by: Greg Lennon, Ph.D.
       DNA Sequencing by: Washington University Genome Sequencing Center
       Clone distribution: NCI-CGAP clone distribution information can be
      found through the I.M.A.G.E. Consortium/LLNL at:
     www-bio.lln1.gov/bbrp/image/image.html
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      High quality sequence stop: 260.
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   AUTHOR (AU):
                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                          National Cancer Institute, Cancer Genome Anatomy
Project (CGAP), Tumor Gene Index
Unpublished (1997)
   TITLE (TI):
   JOURNAL (SO):
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                                            modified polylinker; Site-1: Not
I; Site-2: Eco RI; Plasmid DNA
                                             from the normalized library
                                             NCI-CGAP-Kid5 was prepared, and ss
                                             circles were made in vitro.
                                             Following HAP purification, this
                                             DNA was used as tracer in a
                                             subtractive hybridization
                                             reaction. The driver was PCR-amplified cDNAs from a pool of
                                             5,000 clones made from the same
                                             library (cloneIDs 1323912-1325831,
                                             1471368-1472903 and
                                             1492104-1493255). Subtraction by
                                             Bento Soares and M. Fatima
                                            Bonaldo.
SEQUENCE (SEQ):
     1 ttttcctaag gtttaatttt aactaatgaa ttttaaatga tgaatgtaaa gtcaatccaa
   61 gtctttgctt atttgcaatg cacaaactat ttttttgtaa cttgcaggtg aaatacattc
121 ttttcacatg ataatgttt cgcccttatt tatggtcttt tattatttt cttgagtcct
   181 tttccttcaa tagtttaata agtcacttct ggcttgtcta gagagcaatc ctagcacaat
   241 aatgtttcaa cttgcaagga agaacgccct tattgagttg atagaactcc accagctgtt
   301 ttagatctgt aattttgggg tggccatatc caggtgtgtg gaacatttca ccgtcatctt
   361 ctactggtat aattggaaaa gtgctttatt nttttgtcca tgactcttgg accgtaccaa
   421 agttttggg
L2
     ANSWER 136 OF 156
                             GENBANK.RTM. COPYRIGHT 2004 on STN
LOCUS (LOC):
                          AI760945
                                         GenBank (R)
GenBank ACC. NO. (GBN): AI760945
GenBank VERSION (VER): AI760945.1 GI:5176612
CAS REGISTRY NO. (RN): 236076-02-1
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SEQUENCE LENGTH (SQL):
                          312
MOLECULE TYPE (CI):
                          mRNA; linear
DIVISION CODE (CI):
                          Expressed sequence tag
DATE (DATE):
                          21 Dec 1999
DEFINITION (DEF):
                          wi70e05.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone
                          SOURCE:
                          human.
 ORGANISM (ORGN):
                          Homo sapiens
                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                          Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                          Hominidae; Homo
                                   54 c
NUCLEIC ACID COUNT (NA): 90 a
                                          46 g
                                                  122 t
COMMENT:
     Contact: Robert Strausberg, Ph.D.
     Email: cgapbs-r@mail.nih.gov
     Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
     Emmert-Buck, M.D., Ph.D.
       cDNA Library Preparation: M. Bento Soares, Ph.D.
      cDNA Library Arrayed by: Greg Lennon, Ph.D.
      DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be
     found through the I.M.A.G.E. Consortium/LLNL at:
     www-bio.llnl.gov/bbrp/image/image.html
     Insert Length: 403
                            Std Error: 0.00
     Seq primer: -40UP from Gibco.
REFERENCE:
                             (bases 1 to 312)
                          1
                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
   AUTHOR (AU):
                          National Cancer Institute, Cancer Genome Anatomy
Project (CGAP), Tumor Gene Index
Unpublished (1997)
   TITLE (TI):
   JOURNAL (SO):
FEATURES (FEAT):
  Feature Key
                     Location
                                                Qualifier
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source
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                                           /tissue-type="2 pooled tumors
(clear cell type)"
/lab-host="DH10B"
                                           /note="Organ: kidney; Vector:
pT7T3D-Pac (Pharmacia) with a
                                           modified polylinker; Site-1: Not
                                           I; Site-2: Eco RI; Plasmid DNA
                                           from the normalized library
                                           NCI-CGAP-Kid5 was prepared, and ss
                                           circles were made in vitro.
                                           Following HAP purification, this
                                           DNA was used as tracer in a
                                           subtractive hybridization
                                           reaction. The driver was PCR-amplified cDNAs from a pool of
                                           5,000 clones made from the same
                                           library (cloneIDs 1323912-1325831,
                                           1471368-1472903 and
                                           1492104-1493255). Subtraction by
                                           Bento Soares and M. Fatima
                                           Bonaldo.
SEQUENCE (SEQ):
    1 tttcctaagg tttaatttta actaatgaat tttaaatgat gaatgtaaag tcaatccaag 61 tctttgctta tttgcaatgc acaaactatt tttttgtaac ttgcaggtga aatacattct
   121 tttcacatga taacgttttc gcccttattt atggtctttt attattttc ttgagtcctt
   181 ttccttcaat agtttaataa gtcacttctg gcttgtctag agagcaatcc tagcacaata
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   301 tagatctgta aa
L2
     ANSWER 137 OF 156
                            GENBANK.RTM. COPYRIGHT 2004 on STN
LOCUS (LOC):
                          AI695260
                                        GenBank (R)
GenBank ACC. NO. (GBN): A1695260
GenBank VERSION (VER): A1695260.1 GI:4983160
CAS REGISTRY NO. (RN):
                          233989-40-7
SEQUENCE LENGTH (SQL):
                        408
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MOLECULE TYPE (CI):
                            mRNA; linear
DIVISION CODE (CI):
                            Expressed sequence tag
                            16 Dec 1999
DATE (DATE):
DEFINITION (DEF):
                            wa02b08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone
                            IMAGE:2296887 3' similar to TR:Q14449 Q14449
                              ***GRB14***
                                             . ;, mRNA sequence.
SOURCE:
 ORGANISM (ORGN):
                            Homo sapiens
                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                            Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                            Hominidae; Homo
                                      82 c
NUCLEIC ACID COUNT (NA): 112 a
                                              62 q
                                                      152 t
COMMENT:
      Contact: Robert Strausberg, Ph.D.
      Email: cgapbs-r@mail.nih.gov
      Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
      Emmert-Buck, M.D., Ph.D.
       cDNA Library Preparation: M. Bento Soares, Ph.D.
       cDNA Library Arrayed by: Greg Lennon, Ph.D.
       DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be
      found through the I.M.A.G.E. Consortium/LLNL at:
      www-bio.lln1.gov/bbrp/image/image.html
      Insert Length: 848
                             Std Error: 0.00
      Seq primer: -40UP from Gibco
      High quality sequence stop: 396.
                              (bases 1 to 408)
REFERENCE:
                            1
                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
   AUTHOR (AU):
   TITLE (TI):
                            National Cancer Institute, Cancer Genome Anatomy
                            Project (CGAP), Tumor Gené Index
Unpublished (1997)
   JOURNAL (SO):
FEATURES (FEAT):
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                       Location
                                                   Qualifier
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                                               /clone-lib="NCI-CGAP-Kid11"
                                               /lab-host="DH10B"
                                              /note="Organ: kidney; Vector:
pT7T3D-Pac (Pharmacia) with a
                                              modified polylinker; Site-1: Not
I; Site-2: Eco RI; Plasmid DNA
                                              from the normalized library
                                              NCI-CGAP-Kid3 was prepared, and ss
                                              circles were made in vitro.
                                              Following HAP purification, this
                                              DNA was used as tracer in a
                                              subtractive hybridization
                                              reaction. The driver was
PCR-amplified cDNAs from a pool of
                                               5,000 clones made from the same
                                              library (cloneIDs 1322376-1323911, 1456007-1456775, and
                                              1500552-1502855). Subtraction by
                                              Bento Soares and M. Fatima
                                              Bonaldo.
SEQUENCE (SEO):
      1 tcctaaggtt taattttaac taatgaattt taaatgatga atgtaaagtc aatccaagtc
   61 tttgcttatt tgcaatgcac aaactatttt tttgtaactt gcaggtgaaa tacattcttt 121 tcacatgata atgttttcgc ccttatttat ggtctttat tattttctt gagtcctttt 181 ccttcaatag tttaataagt cacttctggc ttgtctagag agcaatccta gcacaataat
   241 gtttcaacti gcaaggaaga acgccctiat tgagttgata gaactccacc agctgtatta
    301 gatetgtaaa tettgtgtgg ceateateea gtgtgtggaa eattteaceg teatetteta
   361 cccatccaca agtccttgct gaataatcaa tcgctgagcc tcatctta
L2
     ANSWER 138 OF 156
                              GENBANK.RTM. COPYRIGHT 2004 on STN
LOCUS (LOC):
                            AI671320
                                           GenBank (R)
GenBank ACC. NO. (GBN): AI671320
GenBank VERSION (VER):
                            AI671320.1 GI:4851051
CAS REGISTRY NO. (RN):
                            232699-27-3
SEQUENCE LENGTH (SQL):
                            497
MOLECULE TYPE (CI):
                           mRNA: linear
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DIVISION CODE (CI):
                             Expressed sequence tag
DATE (DATE):
                             17 Dec 1999
DEFINITION (DEF):
                             wc29a02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone
                             IMAGE:2316554 3' similar to TR:Q14449 Q14449 ***GRB14*** .;, mRNA sequence.
SOURCE:
                              human.
 ORGANISM (ORGN):
                             Homo sapiens
                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                             Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                             Hominidae; Homo
NUCLEIC ACID COUNT (NA): 144 a
                                        100 c
                                                  87 g
                                                           164 t
                                                                    2 others
COMMENT:
      Contact: Robert Strausberg, Ph.D.
      Email: cgapbs-r@mail.nih.gov
      Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
      Emmert-Buck, M.D., Ph.D.
       cDNA Library Preparation: M. Bento Soares, Ph.D.
       cDNA Library Arrayed by: Greg Lennon, Ph.D.
       DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be
      found through the I.M.A.G.E. Consortium/LLNL at:
      www-bio.llnl.gov/bbrp/image/image.html
      Insert Length: 795
                               Std Error: 0.00
      Seg primer: -40UP from Gibco
      High quality sequence stop: 372.
                             1 (bases 1 to 497)
REFERENCE:
   AUTHOR (AU):
                             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
    TITLE (TI):
                             National Cancer Institute, Cancer Genome Anatomy
                             Project (CGAP), Tumor Gene Index
Unpublished (1997)
    JOURNAL (SO):
FEATURES (FEAT):
  Feature Key
                        Location
                                                      Qualifier
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                   1..497
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                                                 /db-xref="taxon:9606"
                                                 /clone="IMAGE:2316554"
/clone-lib="NCI-CGAP-Kid11"
                                                 /lab-host="DH10B'
                                                 /note="Organ: kidney; Vector:
pT7T3D-Pac (Pharmacia) with a
                                                 modified polylinker; Site-1: Not
I; Site-2: Eco RI; Plasmid DNA
                                                 from the normalized library
                                                 NCI-CGAP-Kid3 was prepared, and ss
                                                 circles were made in vitro.
                                                 Following HAP purification, this
                                                 DNA was used as tracer in a
                                                 subtractive hybridization
                                                 reaction. The driver was PCR-amplified cDNAs from a pool of
                                                 5,000 clones made from the same
                                                 library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by
                                                 Bento Soares and M. Fatima
                                                 Bonaldo.
SEQUENCE (SEO):
   1 gcctgccagt gacacataaa tatcactatt gccaaattcg ctaaaaactg caaatgccgc 61 ggttcctttg atgttccttt agtagaaaaa tataaaccag atcttcttag aaaaaagtaa 121 attttttcc aagacttctt tccctgttct ttcgcatgta agaaaccatg aatttcagga 181 tatgtgcttg aactcagaaa catctgcaaa atctgtgtgg gggatatttc accattggtt tcagttgcaa aagataccat atgctctgga aaaaaataca ttgggtttt aaagaaactca
    301 tatitggcat aaittittet aaagtatagt tigittett etictateee eeagtiggat
   361 agcacttcaa tcaccagttc gtggtcttct attgttcttt ctacacctat gtgaggcagg
   421 tgctcanaaa gggtccagct gtggtcatca atgtaatgat tcttcaggat caacagctga
   481 ncaacatctc gagccgt
L2
     ANSWER 139 OF 156
                                GENBANK.RTM. COPYRIGHT 2004 on STN
LOCUS (LOC):
                             AI624682
                                             GenBank (R)
GenBank ACC. NO. (GBN): AI624682
GenBank VERSION (VER): A1624682.1 GI:4649613
CAS REGISTRY NO. (RN): 230649-94-2
SEQUENCE LENGTH (SQL): 533
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MOLECULE TYPE (CI):
                         mRNA; linear
                         Expressed sequence tag
DIVISION CODE (CI):
DATE (DATE):
                         14 Dec 1999
DEFINITION (DEF):
                         ts43e12.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone
                         IMAGE:2231374 3' similar to TR:Q14449 Q14449
                           ***GRB14***
                                        . ;, mRNA sequence.
SOURCE:
 ORGANISM (ORGN):
                         Homo sapiens
                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                         Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                         Hominidae; Homo
NUCLEIC ACID COUNT (NA): 144 a
                                  104 c
                                          91 q
                                                 193 t
                                                          1 others
COMMENT:
     Contact: Robert Strausberg, Ph.D.
     Email: cgapbs-r@mail.nih.gov
     Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
     Emmert-Buck, M.D., Ph.D.
      cDNA Library Preparation: Life Technologies, Inc.
      CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
      Clone distribution: NCI-CGAP clone distribution information can be
     found through the I.M.A.G.E. Consortium/LLNL at:
     www-bio.llnl.gov/bbrp/image/image.html
     Insert Length: 1696
                           Std Error: 0.00
     Seq primer: -40UP from Gibco
     High quality sequence stop: 401
     POLYA=No.
REFERENCE:
                         1 (bases 1 to 533)
                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
   AUTHOR (AU):
                        National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
   TITLE (TI):
   JOURNAL (SO):
                        Unpublished (1997)
FEATURES (FEAT):
  Feature Key
                    Location
                                             Qualifier
source
                1..533
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                                         /db-xref="taxon:9606'
                                         /clone="IMAGE:2231374"
                                         /clone-lib="NCI-CGAP-Ut1"
/tissue-type="well-differentiated
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                                         pooled tumors"
                                         /lab-host="DH10B"
                                         /note="Organ: uterus; Vector:
                                         pCMV-SPORT6; Site-1: SalI; Site-2:
                                         NotI; Cloned unidirectionally.
                                         Primer: Oligo dT. Average insert
                                         size 1.75 kb. Life Technologies
                                         catalog #: 11538-014
SEQUENCE (SEQ):
     1 tcctaaggtt taattttaac taatgaattt taaatgatga atgtaaagtc aatccaagtc
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   121 tcacatggta atgttticgc ccttatttat ggtcttttat tatitttctt gagtcctttt
   181 ccttcaatag tttaataagt cacttctggc ttgtctagag agcaatccta gcacaataat
   241 gtttcaactt gcaaggaaga acgcccttat tgagttgata gaactccacc agctgtatta
   301 gatetgtaaa tettgtgtgg eeateateea gtgtgtggaa eattteaceg teatetteta
   361 ctggtataat ttgaaagtgc tttatttttt gtccatgact cattgacagt acgaaagttt
   421 tggggttact ctgactatcc cgtaccaaga aaactccatc cacaagtcct tgctgaataa
   481 tcaatcgctg agcctcatct ctagaaatnt tgtgtgaacc atggctggga ccg
L2
     ANSWER 140 OF 156
                          GENBANK.RTM. COPYRIGHT 2004 on STN
LOCUS (LOC):
                        AI610228
                                      GenBank (R)
GenBank ACC. NO. (GBN): AI610228
GenBank VERSION (VER):
                        AI610228.1 GI:4619395
                         390132-63-5
CAS REGISTRY NO. (RN):
SEQUENCE LENGTH (SQL):
                        701
MOLECULE TYPE (CI):
                        mRNA; linear
DIVISION CODE (CI):
                        Expressed sequence tag
DATE (DATE):
                        13 May 1999
DEFINITION (DEF):
                        tp15g09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone
                        IMAGE: 2187904 3' similar to TR: Q14449 Q14449
                           ***GRB14*** . ;, mRNA sequence.
SOURCE:
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ORGANISM (ORGN):
                              Homo sapiens
                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                              Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                              Hominidae; Homo
NUCLEIC ACID COUNT (NA): 179 a
                                          144 c
                                                    132 g
                                                              242 t
                                                                        4 others
COMMENT:
       Contact: Robert Strausberg, Ph.D.
      Email: cgapbs-r@mail.nih.gov
      Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
      Emmert-Buck, M.D., Ph.D.
        cDNA Library Preparation: Life Technologies, Inc.
       cDNA Library Arrayed by: Greg Lennon, Ph.D.
       DNA Sequencing by: Washington University Genome Sequencing Center
        Clone distribution: NCI-CGAP clone distribution information can be
      found through the I.M.A.G.E. Consortium/LLNL at:
      www-bio.lln1.gov/bbrp/image/image.html
      Insert Length: 803
                               Std Error: 0.00
      Seq primer: -40UP from Gibco
      High quality sequence stop: 406
      POLYA=No.
REFERENCE:
                              1 (bases 1 to 701)
                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
    AUTHOR (AU):
                              National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
    TITLE (TI):
                              Unpublished (1997)
    JOURNAL (SO):
FEATURES (FEAT):
   Feature Key
                         Location
                                                       Qualifier
1..701
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source
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                                                   /clone-lib="NCI-CGAP-Gas4"
                                                   /tissue-type="poorly
                                                   differentiated adenocarcinoma with
                                                  signet ring cell features"
/lab-host="DH108"
                                                   /note="Organ: stomach; Vector:
                                                   pCMV-SPORT6; Site-1: SalI; Site-2:
                                                   NotI; Cloned unidirectionally.
                                                  Primer: Oligo dT. Average insert size 1.69 kb. Life Technologies
                                                  catalog #: 11549-011
SEQUENCE (SEQ):
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    121 tcacatggta atgttticgc ccttatttat ggtcttttat tattittctt gagtcctttt
    181 ccttcaatag tttaataagt cacttctggc ttgtctagag agcaatccta gcacaataat
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    661 ggattttcta taactctgct tttctggcct gagaagtcca t
L2
      ANSWER 141 OF 156
                                GENBANK.RTM. COPYRIGHT 2004 on STN
LOCUS (LOC):
                              AI609572
                                              GenBank (R)
GenBank ACC. No. (GBN): AI609572
GenBank VERSION (VER):
                              AI609572.1 GI:4618739
CAS REGISTRY NO. (RN):
                              230319-99-0
SEQUENCE LENGTH (SQL):
                              368
MOLECULE TYPE (CI):
                              mRNA: linear
DIVISION CODE (CI):
                              Expressed sequence tag
DATE (DATE):
                              14 May 1999
DEFINITION (DEF):
                              tw28a08.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone
                              IMAGE:2260982 3' similar to TR:Q14449 Q14449
                                 ***GRB14***
                                                . ;, mRNA sequence.
SOURCE:
 ORGANISM (ORGN):
                              Homo sapiens
                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                              Hominidae: Homo
```

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NUCLEIC ACID COUNT (NA): 100 a
                                   59 c
                                           57 g
                                                 151 t
                                                           1 others
COMMENT:
     Contact: Robert Strausberg, Ph.D.
     Email: cgapbs-r@mail.nih.gov
     Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
     R. Emmert-Buck, M.D., Ph.D.
      cDNA Library Preparation: Life Technologies, Inc.
      cDNA Library Arrayed by: Greg Lennon, Ph.D.
      DNA Sequencing by: Washington University Genome Sequencing Center
     Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
     Insert Length: 318
                           ˈStd Ĕrror: 0.00
     Seq primer: -40UP from Gibco
     High quality sequence stop: 324
     POLYA=No.
                          1 (bases 1 to 368)
REFERENCE:
   AUTHOR (AU):
                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
   TITLE (TI):
                          National Cancer Institute, Cancer Genome Anatomy
                          Project (CGAP), Tumor Gene Index
   JOURNAL (SO):
                          Unpublished (1997)
FEATURES (FEAT):
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                     Location
                                                Qualifier
___________
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source
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                                            description)"
                                            /lab-host="DH10B"
                                           /note="Organ: ovary; Vector: pCMV-SPORT6; Site-1: SalI; Site-2:
                                           NotI; This library represents the
                                           normalized version of
                                           NCI-CGAP-Ov23. Cloned
                                            unidirectionally. Primer: Oligo
                                            dT. Average insert size 0.86 kb.
                                           Tumor types include: mixed
                                           Mullerian tumor, papillary serous, clear cell, spindle cell. All are
                                                                         All are
                                            primary tumors, metastasis
                                            positive. Constructed by Life
                                            Technologies.'
SEQUENCE (SEQ):
     1 tttttttttt ttttttttt ttttttatgc atacacttct tggatttatt aatgctatag
    61 ttctatgaaa tccatgagta aatatagaaa cattgaaatt ccttctctct ctttagagtt
   121 ttcttggtac gggatagtca gagtaacccc aaaactttcg tactgtcaat gagtcatgga
   181 caaaaaataa agcactttca aattatacca gtaagtaatt cgtgatttca catttgtgta
   241 ttagaaatga ccttaatgct aagcttttga tcttaatgca taagcttttg gaaactttgg 301 ttttcttttg gncttttat taaatataat ttggcagctt gtgctttgac tagagccccg
   361 cgtccgcc
L2
     ANSWER 142 OF 156
                            GENBANK.RTM.
                                           COPYRIGHT 2004 on STN
                          AI522272
LOCUS (LOC):
                                        GenBank (R)
GenBank ACC. NO. (GBN): AI522272
                                       GI:4436407
GenBank VERSION (VER):
                          AI522272.1
                          228602-27-5
CAS REGISTRY NO. (RN):
SEQUENCE LENGTH (SQL): MOLECULE TYPE (CI):
                          604
                          mRNA; linear
DIVISION CODE (CI):
                          Expressed sequence tag
DATE (DATE)
                          13 Apr 1999
DEFINITION (DEF):
                          ti84g01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone
                          IMAGE:2138736 3' similar to TR:Q14449 Q14449
                            ***GRB14*** . ;, mRNA sequence.
SOURCE:
                          human.
ORGANISM (ORGN):
                          Homo sapiens
                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                          Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                          Hominidae; Homo
NUCLEIC ACID COUNT (NA): 160 a
                                    118 c
                                            118 g
                                                     208 t
COMMENT:
     Contact: Robert Strausberg, Ph.D.
```

```
Email: cgapbs-r@mail.nih.gov
      Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
      Emmert-Buck, M.D., Ph.D.
       cDNA Library Preparation: M. Bento Soares, Ph.D.
       cDNA Library Arrayed by: Greg Lennon, Ph.D.
       DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be
      found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
      Insert Length: 1380
                                 Std Error: 0.00
      Seq primer: -40UP from Gibco
      High quality sequence stop: 308.
REFERENCE:
                                 (bases 1 to 604)
   AUTHOR (AU):
                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
   TITLE (TI):
                              National Cancer Institute, Cancer Genome Anatomy
                              Project (CGAP), Tumor Gené Index
   JOURNAL (SO):
                              Unpublished (1997)
FEATURES (FEAT):
                                                      Qualifier
  Feature Key
                        Location
 /organism="Homo sapiens"
/db-xref="taxon:9606"
                   1..604
source
                                                  /clone="IMAGE:2138736"
                                                  /clone-lib="NCI-CGAP-Kid11"
                                                  /lab-host="DH10B"
                                                  /note="Organ: kidney; Vector:
                                                  pT7T3D-Pac (Pharmacia) with a
                                                  modified polylinker; Site-1: Not
I; Site-2: Eco RI; Plasmid DNA
from the normalized library
                                                  NCI-CGAP-Kid3 was prepared, and ss circles were made in vitro.
                                                  Following HAP purification, this
                                                  DNA was used as tracer in a
                                                  subtractive hybridization
                                                  reaction. The driver was
                                                  PCR-amplified cDNAs from a pool of
                                                  5,000 clones made from the same
                                                  library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by
                                                  Bento Soares and M. Fatima
                                                  Bonaldo.
SEQUENCE (SEQ):
      1 ttcctaaggt ttaattttaa ctaatgaatt ttaaatgatg aatgtaaagt caatccaagt
     61 ctttgcttat ttgcaatgca caaactattt ttttgtäact tgcaggtgaa atacattctt
    121 ttcacatgat aatgttticg cccttattta tggtčtttta třatřitict tgagtccttt
   181 tccttcaata gtttaataag tcacttctgg cttgtctaga gagcaatcct agcacaataa 241 tgtttcaact tgcaaggaag aacgcctta ttgagttgat agaactccac cagctgtatt 301 agatctgtaa atcttgtgtg gccatcatcc agtgtgtgga acatttcacc gtcatcttct 361 actggtataa tttgaaagtg ctttattttt tgtccatgac tcattgacag tacgaaagtt 421 ttgggggtaca tctgactatc ccgtaccaag aaaactccat ccacaagtcc ttgctgaata
    481 atcaatcgct gagcctcatc tctagaaatt ttgtggtgaa accatggctg ggacccgtgg
    541 atagccatgt tigtggcaaa gctictggaa gaggcagggg ggctccggga gigcccaggc
   601 qtaa
      ANSWER 143 OF 156
                                GENBANK.RTM. COPYRIGHT 2004 on STN
LOCUS (LOC):
                              AI505286
                                              GenBank (R)
GenBank ACC. NO. (GBN): AI505286
GenBank VERSION (VER):
                              AI505286.1 GI:4403137
CAS REGISTRY NO. (RN):
                              228210-72-8
SEQUENCE LENGTH (SQL):
                              578
MOLECULE TYPE (CI):
                              mRNA: linear
DIVISION CODE (CI):
                              Expressed sequence tag
DATE (DATE):
                              11 Mar 1999
DEFINITION (DEF):
                              vp98h08.x1 Stratagene mouse diaphragm (#937303) Mus
                              musculus cDNA clone IMAGE:1092831 3 similar to TR:Q14449 Q14449 ***GRB14*** . ;, mRNA sequence.
SOURCE:
                              house mouse.
                             Mus musculus
 ORGANISM (ORGN):
                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                              Euteleostomi; Mammalia; Eutheria; Rodentia;
```

Sciurognathi; Muridae; Murinae; Mus

L2

```
NUCLEIC ACID COUNT (NA): 148 a
                                          135 c
                                                     111 g
                                                                179 t
                                                                          5 others
COMMENT:
      Contact: Marra M/WashU-NCI Mouse EST Project 1999
      Washington University School of Medicine
      4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
      Tel: 314 286 1800
      Fax: 314 286 1810
      Email: mouseest@watson.wustl.edu
      This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
      This clone was previously sequenced on the 5' end only, this new
      data is from the 3' end
      High quality sequence stop: 379.
                                  (bases 1 to 578)
REFERENCE:
                               Marra,M.; Hillier,L.; Kucaba,T.; Martin,J.; Beck,C.;
    AUTHOR (AU):
                               wylie,T.; Underwood,K.; Steptoe,M.; Theising,B.;
                               Allen,M.; Bowers,Y.; Person,B.; Swaller,T.;
Gibbons,M.; Pape,D.; Harvey,N.; Schurk,R.; Ritter,E.;
Kohn,S.; Shin,T.; Jackson,Y.; Cardenas,M.; McCann,R.;
                               Waterston, R.; Wilson, R.
The WashU-NCI Mouse EST Project 1999
    TITLE (TI):
    JOURNAL (SO):
                               Unpublished (1999)
FEATURES (FEAT):
                         Location
                                                         Qualifier
  Feature Key
  /organism="Mus musculus"
/db-xref="taxon:10090"
/clone="IMAGE:1092831"
/clone-lib="Stratagene mouse
diaphragm (#937303)"
                    1..578
source
                                                    /tissue-type="diaphragm"
/dev-stage="adult"
                                                    /lab-hosť="SOLR (kanamycin
                                                    resistant)"
                                                    /note="Organ: diaphragm; Vector:
                                                    pBluescript SK-; Site-1: EcoRI;
                                                    Site-2: XhoI; Cloned
                                                    unidirectionally from mRNA
                                                    prepared from diaphragm muscle.
                                                    Primer: Oligo dT. Average insert size: 1.5 kb. Uni-ZAP XR Vector;
                                                    ~5' adaptor sequence: 5'
                                                    GAATTCGGCACGAG 3' ~3' adaptor
                                                    sequence: 5
                                                    CTCGAGTTTTTTTTTTTTTTTTTTTTTT
SEQUENCE (SEQ):
      1 aataaggttt aattttaact aataaattta aaggcatgag tgtaatagga atccaagttt
   61 tcactaatti gcaatgtgtg acctatttt tittgtaacc cgcaggtgaa atcttctttt 121 caccatggtt tgttttcagc cttgtgatct ctctctct ctctaatcat tctcctttgc 181 atccttcttc ttctgtagtg taacgagtga cacacagtti ggctaaacag ccatcctagc 241 acagtaatgc ttcagcttgc aaggaaggac cccctgttg agctggtaga actccaccag 301 ctggatgagg tctgtgaact tcgtatggc atcatccaga gtatggaaca gctcaccatc
    361 atcītcīacg ggtatāatnt galagtgītt tatctttīgt ccatgactca itgacagtac
    421 aaaagttetg gggttactet gactateeeg taccaagaaa actneateea caggeeeetg
    481 ccgaatgate agnegetgag ecteatetet tgaaatnetg tggtgaaace catgttggae
    541 cgatggaaac catgttcaca ccanaactct ggaagggc
L2
      ANSWER 144 OF 156
                                  GENBANK.RTM. COPYRIGHT 2004 on STN
LOCUS (LOC):
                               AI494168
                                                GenBank (R)
GenBank ACC. NO. (GBN): AI494168
GenBank VERSION (VER):
                               AI494168.1 GI:4395171
CAS REGISTRY NO. (RN):
                               228132-01-2
SEQUENCE LENGTH (SQL):
                               368
MOLECULE TYPE (CI):
                               mRNA; linear
DIVISION CODE (CI):
                               Expressed sequence tag
                               13 Apr 1999
DATE (DATE):
                               ti14f01.y1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2130457 5' similar to TR:Q14449 Q14449 ***GRB14*** :;, mRNA sequence.
DEFINITION (DEF):
SOURCE:
                               Homo sapiens
 ORGANISM (ORGN):
                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
```

```
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                          Hominidae; Homo
NUCLEIC ACID COUNT (NA): 98 a
                                                   141 t
                                   71 c
                                           58 q
COMMENT:
     Contact: Robert Strausberg, Ph.D.
     Email: cgapbs-r@mail.nih.gov
     Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
     Emmert-Buck, M.D., Ph.D.
       cDNA Library Preparation: M. Bento Soares, Ph.D.
       cDNA Library Arrayed by: Greg Lennon, Ph.D.
      DNA Sequencing by: Washington University Genome Sequencing Center
       Clone distribution: NCI-CGAP clone distribution information can be
     found through the I.M.A.G.E. Consortium/LLNL at:
     www-bio.llnl.gov/bbrp/image/image.html
     Insert Length: 416
                             Std Error: 0.00
     Seq primer: -40RP from Gibco.
                             (bases 1 to 368)
REFERENCE:
   AUTHOR (AU):
                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                          National Cancer Institute, Cancer Genome Anatomy
   TITLE (TI):
                           Project (CGAP), Tumor Gene Index
   JOURNAL (SO):
                          Unpublished (1997)
FEATURES (FEAT):
                      Location
                                                 Oualifier
  Feature Key
 __________
                                             /organism="Homo sapiens"
                 1..368
source
                                             /db-xref="taxon:9606"
                                             /clone="IMAGE:2130457"
                                             /clone-lib="NCI-CGAP-Kid11"
                                             /lab-host="DH10B
                                             /note="Organ: kidney; Vector:
pT7T3D-Pac (Pharmacia) with a
                                            modified polylinker; Site-1: Not
I; Site-2: Eco RI; Plasmid DNA
                                             from the normalized library
                                             NCI-CGAP-Kid3 was prepared, and ss
                                             circles were made in vitro.
                                             Following HAP purification, this
                                             DNA was used as tracer in a
                                             subtractive hybridization
                                             reaction. The driver was PCR-amplified cDNAs from a pool of
                                             5,000 clones made from the same
                                             library (cloneIDs 1322376-1323911,
                                             1456007-1456775, and
                                             1500552-1502855). Subtraction by
                                             Bento Soares and M. Fatima
                                             Bonaldo.
SEQUENCE (SEQ):
   1 tcctaaggtt taattttaac taatgaattt taaatgatga atgtaaagtc aatccaagtc 61 tttgcttatt tgcaatgcac aaactatttt tttgtaactt gcaggtgaaa tacattcttt 121 tcacatgata atgttttcgc ccttatttat ggtcttttat tattttctt gagtccttt
   181 ccttcaatag tttaataagt cacttctggc ttgtctagag agcaatccta gcacaataat
   241 gtttcaacti gcaaggaaga acgccctiat tgagttgata gaactccacc agctgtatta
   301 gatetgtaaa tettgtgtgg ceateateea gtgtgtggaa eattteaceg teatettete
   361 ctcgtgcc
L2
     ANSWER 145 OF 156
                             GENBANK.RTM. COPYRIGHT 2004 on STN
LOCUS (LOC):
                          AI425417
                                         GenBank (R)
GenBank ACC. NO. (GBN): AI425417
GenBank VERSION (VER):
                           AI425417.1 GI:4271348
CAS REGISTRY NO. (RN):
                           226504-01-4
SEQUENCE LENGTH (SQL):
                           503
                           mRNA; linear
MOLECULE TYPE (CI):
DIVISION CODE (CI):
                           Expressed sequence tag
DATE (DATE):
                           15 Mar 2000
                          my18a09.y1 Barstead mouse heart MPLRB3 Mus musculus cDNA clone IMAGE:696184 5' similar to TR:Q14449 Q14449 ***GRB14*** . ;, mRNA sequence.
DEFINITION (DEF):
                                           . ;, mRNA sequence.
SOURCE:
                           house mouse.
 ORGANISM (ORGN):
                          Mus musculus
                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                           Euteleostomi; Mammalia; Eutheria; Rodentia;
```

Sciurognathi; Muridae; Murinae; Mus

```
NUCLEIC ACID COUNT (NA): 103 a 171 c
                                                  143 q
                                                            86 t
COMMENT:
      Contact: Marra M/WashU-NCI Mouse EST Project 1999
      Washington University School of Medicine
      4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
      Tel: 314 286 1800
      Fax: 314 286 1810
      Email: mouseest@watson.wustl.edu
     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the
      correct orientation)
      MGI:429744
      Seq primer: -40RP from Gibco
      High quality sequence stop: 493
      POLYA=No.
REFERENCE:
                             1 (bases 1 to 503)
                             Marra,M.; Hillier,L.; Kucaba,T.; Martin,J.; Beck,C.; Wylie,T.; Underwood,K.; Steptoe,M.; Theising,B.; Allen,M.; Bowers,Y.; Person,B.; Swaller,T.; Gibbons,M.; Pape,D.; Harvey,N.; Schurk,R.; Ritter,E.;
   AUTHOR (AU):
                             Kohn, S.; Shin, T.; Jackson, Y.; Cardenas, M.; McCann, R.;
                             Waterston, R.; Wilson, R.
   TITLE (TI):
                             The WashU-NCI Mouse EST Project 1999
   JOURNAL (SO):
                             Unpublished (1999)
FEATURES (FEAT):
                       Location
                                                      Qualifier
  Feature Key
_____+
                                                 /organism="Mus musculus"
                                                 /strain="BALB/c"
/db-xref="taxon:10090"
                                                 /clone="IMAGE:696184"
                                                 /clone-lib="Barstead mouse heart
                                                 MPLRB3"
                                                 /sex="mixed"
                                                 /tissue-type="heart"
/dev-stage="6 weeks"
                                                 /lab-host="DH10B'
                                                 /note="Organ: heart; Vector:
                                                 pT7T3D-Pac (Pharmacia) with a
                                                 modified polylinker; Site-1: ECORI; Site-2: NotI; 1st strand
                                                 cDNA was primed with a Not I -
                                                 oligo(dT) primer [5
                                                 TGTTACGAATCTGAAGTGGGAGCGGCCCCTTT
                                                 to Eco RI adaptors
                                                 [CTTGGATTCGGTACC], digested with Not I and cloned into the Not I and Eco RI sites of the modified
                                                 pT7T3 vector. Library constructed
                                                 by Bob Barstead."
SEQUENCE (SEQ):
      1 aatteggate caaggeaagg egetegetge etgeaacege teggetetge tegeceecag
     61 cccttcgtag ctttcgcctc gcggtcgatg actccctaga cccctggcct acgaccatga
   181 tggcagtgca ggtgtgccgc gttgcccagg gcaagggaga cgcccaggac ccggcgcagg
241 tccccggact gcacgcgctg tcccccgct ccgatgcgac cctccgcggt gccatagaca
   301 ggagaaaaat gaaagatctg gatgttctgg aaaagccacc cattcccaac ccctttcctg 361 agctctgctg ctctccgctt acatctgtgc tgtcagcagg cctgtttccc agggccaatt
   421 caaggaagaa gcaggtgatt aaagtttaca gcgaggatga aaccagcaga gcattagagg
   481 tgcccagtga catcacagcc cga
L2
     ANSWER 146 OF 156
                                GENBANK.RTM. COPYRIGHT 2004 on STN
LOCUS (LOC):
                             AI383743
                                             GenBank (R)
GenBank ACC. NO. (GBN): AI383743
GenBank VERSION (VER):
                             AI383743.1 GI:4196524
                             225333-52-8
CAS REGISTRY NO. (RN):
SEQUENCE LENGTH (SQL):
                             423
MOLECULE TYPE (CI):
                             mRNA; linear
DIVISION CODE (CI):
                             Expressed sequence tag
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18 Mar 1999
DATE (DATE):
DEFINITION (DEF):
                         tc47e05.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens
                         cDNA clone IMAGE:2067776 3' similar to TR:Q14449 Q14449
                           ***GRB14***
                                         . ;, mRNA sequence.
SOURCE:
ORGANISM (ORGN):
                         Homo sapiens
                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                         Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                         Hominidae; Homo
116 a 74 c
NUCLEIC ACID COUNT (NA): 116 a
                                         69 g
                                                 162 t 2 others
COMMENT:
     Contact: Robert Strausberg, Ph.D.
     Email: cgapbs-r@mail.nih.gov
     This clone is available royalty-free through LLNL; contact the
     IMAGE Consortium (info@image.llnl.gov) for further information.
     Insert Length: 967
                           Std Error: 0.00
     Seq primer: -40UP from Gibco.
REFERENCE:
                         1 (bases 1 to 423)
                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
   AUTHOR (AU):
                         National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
   TITLE (TI):
                         Unpublished (1997)
   JOURNAL (SO):
FEATURES (FEAT):
  Feature Key
                   Location
                                             Qualifier
/organism="Homo sapiens"
/db-xref="taxon:9606"
/clone="IMAGE:2067776"
                1..423
source
                                          /clone-lib="Soares-total-fetus-Nb2
HF8-9w"
                                          /dev-stage="8-9 weeks"
                                          /lab-host="DH10B"
                                          /note="Vector: pT7T3D-Pac
                                          (Pharmacia) with a modified
                                          polylinker; Site-1: Not I; Site-2:
                                          Eco RI; 1st strand cDNA was
                                          prepared from mRNA obtained from
                                          pooled 8-9 week (total) fetus
                                          material with a Not I - oligo(dT)
                                          primer [5'
                                          TGTTACCĀATCTGAAGTGGGAGCGGCCGCTTAAT
                                          TTTTTTTTTTTTTT 3'].
                                          Double-stranded cDNA was ligated
                                          to Eco RI adaptors (Pharmacia),
                                          digested with Not I and cloned
                                          into the Not I and Eco RI sites of
                                          the modified pT7T3 vector. Library
                                          went through one round of
                                          normalization, and was constructed
                                           by Bento Soares and M. Fatima
                                          Bonaldo.
SEQUENCE (SEQ):
     1 cctaaggttt aattttaact aatgaatttt aaatgatgaa tgtaaagtca atccaagtct
    61 ttgcttattt gcaatgcaca aactatttt ttgtaacttg caggtgaaat acattctttt
   121 cacatgataa cgtttīcgcc cttatttatg gtčttttatī atīītīcttg agtccttttc
   181 cttcaatagt ttaataagtc acttctggct tgtctagaga gcaatcctag cacaataatg
   241 tttcaacttg caaggaagaa cgcccttatt gagttgatag aactccacca gctgtattag 301 atctgtaaat cttgtgtggc catcatccag tgtgtggaac atttcaccgt catcttctac
   361 tggtátaatt ngaáagtgót ttattnttti gicatgáctc attgacagia caaaagtttt
   421 ggg
                           GENBANK.RTM. COPYRIGHT 2004 on STN
L2
     ANSWER 147 OF 156
LOCUS (LOC):
                         AI364971
                                       GenBank (R)
GenBank ACC. No. (GBN): AI364971
GenBank VERSION (VER):
                         AI364971.1 GI:4124660
CAS REGISTRY NO. (RN):
                         224494-55-7
SEQUENCE LENGTH (SQL):
                         318
MOLECULE TYPE (CI):
                         mRNA; linear
DIVISION CODE (CI):
                         Expressed sequence tag
                         16 Feb 1999
DATE (DATE):
DEFINITION (DEF):
                         qz41h03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone
                         IMAGE:2029493 3' similar to TR:Q14449 Q14449 ***GRB14*** . ;, mRNA sequence.
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ORGANISM (ORGN):
                         Homo sapiens
                         Eukaryota; Metazoa; Chordata; Craniata: Vertebrata;
                          Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                         Hominidae; Homo
NUCLEIC ACID COUNT (NA): 90 a
                                  54 c
                                         48 g
                                                 125 t
                                                          1 others
COMMENT:
     Contact: Robert Strausberg, Ph.D.
     Email: cgapbs-r@mail.nih.gov
     Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
     Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D.
      cDNA Library Arrayed by: Greg Lennon, Ph.D.
      DNA Sequencing by: Washington University Genome Sequencing Center
      Clone distribution: NCI-CGAP clone distribution information can be
     found through the I.M.A.G.E. Consortium/LLNL at:
     www-bio.llnl.gov/bbrp/image/image.html
     Insert Length: 447
                           Std Error: 0.00
     Seq primer: -40UP from Gibco.
                         1 (bases 1 to 318)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
REFERENCE:
   AUTHOR (AU):
                         National Cancer Institute, Cancer Genome Anatomy
Project (CGAP), Tumor Gene Index
   TITLE (TI):
                         Unpublished (1997)
   JOURNAL (SO):
FEATURES (FEAT):
                                               Qualifier
  Feature Key
                     Location
/organism="Homo sapiens"
                 1..318
source
                                           /db-xref="taxon:9606
                                           /clone="IMAGE:2029493"
/clone-lib="NCI-CGAP-Kid11"
                                           /lab-host="DH10B"
                                           /note="Organ: kidney; Vector:
                                           pT7T3D-Pac (Pharmacia) with a
                                           modified polylinker; Site-1: Not
                                           I; Site-2: Eco RI; Plasmid DNA
                                           from the normalized library
                                           NCI-CGAP-Kid3 was prepared, and ss circles were made in vitro.
                                          Following HAP purification, this DNA was used as tracer in a subtractive hybridization
                                           reaction. The driver was
                                           PCR-amplified cDNAs from a pool of
                                           5,000 clones made from the same
                                           library (cloneIDs 1322376-1323911, 1456007-1456775, and
                                           1500552-1502855). Subtraction by
                                           Bento Soares and M. Fatima
                                           Bonaldo.
SEQUENCE (SEQ):
     1 ttcctaaggt ttaattttaa ctaatgaatt ttaaatgatg aatgtaaagt caatccaagt
    61 ctttgctťat ttgcaatgca caaacťattt ttttgtaacť tgcaggtgaa atacattcťt
   121 ttcacatgat aatgttticg cccttattta tggnčtttta tťatiťtťct tgagtccttt
   181 teetteaata gittaataag teaetietgg ettgietaga gageaateet ageacaataa
   241 tgtttcaact tgcaaggaag aacgccctta ttgagttgat agaactccac cagctgtatt
   301 agatctgtaa atcttgtg
L2
     ANSWER 148 OF 156
                            GENBANK.RTM. COPYRIGHT 2004 on STN
LOCUS (LOC):
                          AI263214
                                       GenBank (R)
GenBank ACC. NO. (GBN): AI263214
GenBank VERSION (VER):
                          AI263214.1 GI:3871417
                          221598-25-0
CAS REGISTRY NO. (RN):
SEQUENCE LENGTH (SQL):
                          382
MOLECULE TYPE (CI):
                          mRNA; linear
DIVISION CODE (CI):
                          Expressed sequence tag
DATE (DATE):
                          3 Feb 1999
DEFINITION (DEF):
                          qz36f04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone
                          IMAGE:2028991 3' similar to TR:Q14449 Q14449
                            ***GRB14***
                                         . ;, mRNA sequence.
SOURCE:
                          Homo sapiens
 ORGANISM (ORGN):
                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
```

SOURCE:

human.

```
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                           Hominidae; Homo
NUCLEIC ACID COUNT (NA): 112 a
                                      59 с
                                             56 g
                                                    154 t
                                                              1 others
COMMENT:
     Contact: Robert Strausberg, Ph.D.
     Email: cgapbs-r@mail.nih.gov
     Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
     Emmert-Buck, M.D., Ph.D.
       cDNA Library Preparation: M. Bento Soares, Ph.D.
      cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
      found through the I.M.A.G.E. Consortium/LLNL at:
     www-bio.llnl.gov/bbrp/image/image.html
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     Seq primer: -40UP from Gibco
     High quality sequence stop: 381.
REFERENCE:
                           1 (bases 1 to 382)
   AUTHOR (AU):
                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                           National Cancer Institute, Cancer Genome Anatomy
Project (CGAP), Tumor Gene Index
   TITLE (TI):
                           Unpublished (1997)
   JOURNAL (SO):
FEATURES (FEAT):
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                      Location
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                                             modified polylinker; Site-1: Not
I; Site-2: Eco RI; Plasmid DNA
                                              from the normalized library
                                              NCI-CGAP-Kid3 was prepared, and ss
                                              circles were made in vitro.
                                              Following HAP purification, this
                                              DNA was used as tracer in a
                                              subtractive hybridization
                                             reaction. The driver was PCR-amplified cDNAs from a pool of
                                              5,000 clones made from the same
                                              library (cloneIDs 1322376-1323911, 1456007-1456775, and
                                              1500552-1502855). Subtraction by
                                              Bento Soares and M. Fatima
                                              Bonaldo.
SEQUENCE (SEQ):
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121 caggggaaat acattcttt cacatgataa tgttttcgcc cttatttatg gtcttttatt
   181 attiticttg agtccttttc cttcaatagt ttaataagtc acttctggct tgtctagaga
   241 gcaatcctag cacaataatg tttcaactig caaggaaaaa cgccctiatt gagttgatag
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   361 gggttttnaa aaaaaaaaa aa
L2
     ANSWER 149 OF 156
                             GENBANK.RTM. COPYRIGHT 2004 on STN
LOCUS (LOC):
                           AF076619
                                          GenBank (R)
GenBank ACC. NO. (GBN): AF076619
GenBank VERSION (VER):
                           AF076619.1 GI:3650499
CAS REGISTRY NO. (RN):
                           216295-93-1
SEQUENCE LENGTH (SQL):
                           1950
MOLECULE TYPE (CI):
                           mRNA; linear
DIVISION CODE (CI):
                           Rodents
DATE (DATE):
                           26 Sep 1998
DEFINITION (DEF):
                           Rattus norvegicus molecular adapter rGrb14 (
                              ***Grb14*** ) mRNA, complete cds.
SOURCE:
                           Norway rat.
                           Rattus norvegicus
 ORGANISM (ORGN):
                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                           Euteleostomi; Mammalia; Eutheria; Rodentia;
                           Sciurognathi; Muridae; Murinae; Rattus
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NUCLEIC ACID COUNT (NA): 546 a 460 c
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                                1 (bases 1 to 1950)
    AUTHOR (AU):
                                Kasus-Jacobi,A.; Perdereau,D.; Auzan,C.; Clauser,E.;
                                Van Obberghen, E.; Mauvais-Jarvis, F.; Girard, J.;
    TITLE (TI):
                                Identification of the rat adapter ***Grb14***
                                                                                                   as an
                                inhibitor of insulin actions
    JOURNAL (SO):
                                J. Biol. Chem., 273 (40), 26026-26035 (1998)
                                CA 130:20710
    OTHER SOURCE (OS):
                                2 (bases 1 to 1950)
Kasus-Jacobi,A.; Perdereau,D.; Burnol,A.-F.
REFERENCE:
    AUTHOR (AU):
    TITLE (TI):
                                Direct Submission
                                Submitted (03-JUL-1998) UPR 1524, CNRS, 9 rue Jules
    JOURNAL (SO):
                                Hetzel, Meudon 92190, France
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                                                      LKNHYVDDNSWTLFEHLSHTGVER
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                                                      YFFLRRSGLYFSTKGTSKEPRHLQ
                                                      FFSEFSTSNVYMSLAGKKKHGAPTPYGFCFKPTK
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                                                      IRLLKYGMQLYQNYMHPSQARSACSSQSVSPMRS
                                                      VSENSLVAMDFSGQKTRVIDNPTE
                                                      ALSVAVEEGLAWRKKGCLRLGNHGSPTAPSQSSA
                                                      VNMALHRSQPWFHHRISRDEAQQL
                                                      ITRQGPVDGVFLVRDSQSNPRTFVLSMSHGQKIK
                                                     HFQIIPVEDDGEVFHTLDDGHTKF
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SEQUENCE (SEQ):
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    181 gacccggctc aggtccccgg actgcacgcg ctgtccccgg cctcagatgc gacccgccgc 241 ggtgccatgg acaggagaaa agcgaaagat ctggaagttc aggaaacgcc ttccattcct
    301 aaccccttcc ctgagctctg ctgttctcca cttacatcgg tgctgtcagc aggcctcttc
    361 cccagatcaa attcaaggaa gaaacaggtg attaaagttt acagcgagga tgagaccagc
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541 gtagaaagga cagtggagga ccatgagctg ctgactgaag tgctgtctca ttgggtgatg
601 gaagaagata ataagctgta tcttagaaag aattatgcca aatagaatt ttttaagaac
661 ccaatgtatt tctttccaga gcacatgtgt tctttttgaa ccgaaatgaa cggtgacaga
    721 tecettacae agatecegea ggtgttttta ageteaaaea catateetga aateeatgge
    781 ttcctgcatg caaaggaaca ggggaagaag tcttggaaaa aagcttactt ttttctcaga
   841 agatcīggtī tataīītttc tactaaāggc acatccaagg aaccacggca cttgcagtīt
   901 ticagtgaat tcagcactag taatgtttac atgtcactgg caggcaaaaa aaagcatgga
   961 gcgccgactc cctatggatt ctgctttaag cctaccaaag caggagggcc ccgggacctg
  1021 aaaatgctgt gtgcagaaga agaccaaagc aggatgtgct gggtgaccgc cattagattg
1081 ctcaagtatg gcatgcagct ctaccagaat tatatgcatc catccaagc tagaagcgc
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  1261 gttgaggaag gactcgcttg gaggaaaaaa ggatgtttac gcctggggaa tcatgggagt 1321 cccactgcgc cctctcagag ctctgctgtg aacatggctc tccaccggtc ccagccatgg 1381 tttcaccaca gaatttctag agatgaagct cagcagttga ttacccggca ggggcctgtg
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1441 gatggagttt tcttggtacg ggatagtcag agtaacccca gaacttttgt actgtcaatg
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  1561 ttccacaccc tggatgatgg ccatacgaag ttcacagatc tcatccagct cgtggagttc
  1621 taccagetca acaagggggt cetteettge aagetgaage attactgtge taggatgget
  1681 gtttagccaa actgtctgtg actcgttaaa ctatggaaga tggaggatgc aaagaagaat
  1801 tcacaagget ggaaacaaat catggtgaaa agaagattea cetgtgggtt acaaaaaaat
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1921 tattagttaa aattaaacct tattaaaaaa
L2
     ANSWER 150 OF 156
                           GENBANK.RTM. COPYRIGHT 2004 on STN
LOCUS (LOC):
                         AI094433
                                       GenBank (R)
GenBank ACC. NO. (GBN): AI094433
GenBank VERSION (VER):
                         AI094433.1 GI:3433409
CAS REGISTRY NO. (RN):
                         392191-42-3
SEQUENCE LENGTH (SQL):
                         420
MOLECULE TYPE (CI):
                         mRNA; linear
DIVISION CODE (CI):
                         Expressed sequence tag
                         10 Nov 1998
ou87b07.s1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens
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DATE (DATE)
DEFINITION (DEF):
                            ***GRB14*** . ;, mRNA sequence.
SOURCE:
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                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                         Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                         Hominidae; Homo
NUCLEIC ACID COUNT (NA): 115 a
                                   75 c
                                          67 g
                                                  163 t
COMMENT:
     Contact: Robert Strausberg, Ph.D.
     Email: cgapbs-r@mail.nih.gov
     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
     Insert Length: 796
                          Std Error: 0.00
     Seg primer: -40m13 fwd. ET from Amersham
     High quality sequence stop: 277.
                         1 (bases 1 to 420)
REFERENCE:
   AUTHOR (AU):
                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
   TITLE (TI):
                         National Cancer Institute, Cancer Genome Anatomy
                         Project (CGAP), Tumor Gene Index
   JOURNAL (SO):
                         Unpublished (1997)
FEATURES (FEAT):
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                    Location
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                                          /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a
                                          modified polylinker; Site-1: Not
                                          I; Site-2: Eco RI; Equal amounts
                                          of plasmid DNA from five
                                          normalized libraries were mixed.
                                           and ss circles were made in vitro.
                                           Following HAP purification, this
                                          DNA was used as tracer in a
                                           subtractive hybridization
                                          reaction. The driver was PCR-amplified cDNAs from pools of
                                           5,000 clones made from the same 5
                                           libraries. The pools consisted of
                                          the following libraries and
                                           cloneIDs: Soares NbHSF pool 1:
                                           309384-310919, 323208-325895
                                          Soares Nb2HP pool 1:
                                          145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 soares Nb2HF8-9W
                                          pool 1: 758280-760583,
                                          772104-774407 Soares NbHPA pool 1:
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304776-306311, 320136-322823,

326280-326663 Soares NbHOT pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M.

normalization. Library constructed by Bento Soares and M. Fatima

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Fatima Bonaldo.'
SEQUENCE (SEQ):
      f 1 cctaaggttt aattttaact aatgaatttt aaatgatgaa tf gtaaf agtca atccaf agtct
   61 ttgcttattt gcaatgcaca aactatttt ttgtaacttg caggtgaaat acattctttt 121 cacatgataa cgttttcgcc cttatttatg gtcttttatt attttcttg agtccttttc 181 cttcaatagt ttaataagtc acttctggct tgtctagaga gcaatcctag cacaataatg 241 tttcaacttg caaggaagaa cgcccttatt gagttgatag aactccacca gctgtattag
   301 atctgtaaať cttgtgtggc catcatccag tgtgtggaac atttcaccgt catcttctac
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L2
      ANSWER 151 OF 156
                                GENBANK.RTM. COPYRIGHT 2004 on STN
LOCUS (LOC):
                              AA917917
                                              GenBank (R)
GenBank ACC. NO. (GBN): AA917917
GenBank VERSION (VER):
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CAS REGISTRY NO. (RN):
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SEQUENCE LENGTH (SQL):
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MOLECULE TYPE (CI):
                              mRNA; linear
DIVISION CODE (CI):
                              Expressed sequence tag
DATE (DATE):
                              10 Jun 1998
DEFINITION (DEF):
                              ol76q09.s1 NCI_CGAP_Kid3 Homo sapiens cDNA clone
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                                                . ;, mRNA sequence.
SOURCE:
 ORGANISM (ORGN):
                              Homo sapiens
                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                              Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                              Hominidae; Homo
NUCLEIC ACID COUNT (NA): 136 a
                                         95 c
                                                 79 g
                                                          187 t
COMMENT:
      Contact: Robert Strausberg, Ph.D.
      Email: cgapbs-r@mail.nih.gov
      Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
      Emmert-Buck, M.D., Ph.D.
       CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D.
       DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
      found through the I.M.A.G.E. Consortium/LLNL at:
      www-bio.lln1.gov/bbrp/image/image.html
      Insert Length: 664
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REFERENCE:
                                (bases 1 to 497)
   AUTHOR (AU):
                             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
   TITLE (TI):
                             National Cancer Institute, Cancer Genome Anatomy
                             Project (CGAP), Tumor Gene Index
Unpublished (1997)
   JOURNAL (SO):
FEATURES (FEAT):
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                        Location
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modified polylinker; Site-1: Not
I; Site-2: Eco RI; 1st strand cDNA
                                                 was primed with a Not I -
                                                 oligo(dT) primer, double-stranded CDNA was ligated to Eco RI
                                                 adaptors (Pharmacia), digested with Not I and cloned into the Not
                                                 I and Eco RI sites of the
                                                 modified pT7T3 vector. mRNA
source: 2 pooled kidneys. Library
went through one round of
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181 gtcetttee tteaatagtt taataagtea ettetggett gtetagagag caateetage
241 acaataatgt tteaacttge aaggaagaae geeettattg agttgataga acteeaceag
301 etgtattaga tetgtaaate ttgtgtggee ateateeagt gtgtggaaea ttteaeegte
361 atettetaet ggtataattt gaaagtgett tattteetgt ecatgaetea ttgaeagtae
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    481 tgaataatca atcgctg
L2
      ANSWER 152 OF 156
                                 GENBANK.RTM. COPYRIGHT 2004 on STN
LOCUS (LOC):
                              AA684351
                                               GenBank (R)
GenBank ACC. NO. (GBN): AA684351
GenBank VERSION (VER):
                              AA684351.1 GI:2670937
CAS REGISTRY NO. (RN): SEQUENCE LENGTH (SQL):
                              200792-61-6
                              503
MOLECULE TYPE (CI):
                              mRNA; linear
DIVISION CODE (CI):
                              Expressed sequence tag
DATE (DATE):
                              9 Dec 1997
DEFINITION (DEF):
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SOURCE:
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                              Euteleostomi; Mammalia; Euthéria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus
NUCLEIC ACID COUNT (NA): 127 a 121 c
                                                    135 g
COMMENT:
      Contact: Marra M/Mouse EST Project
      WashU-HHMI Mouse EST Project
      Washington University School of MedicineP
      4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
      Tel: 314 286 1800
Fax: 314 286 1810
      Email: mouseest@watson.wustl.edu
      This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
      Possible reversed clone: similarity on wrong strand
      High quality sequence stop: 459.
REFERENCE:
                              1
                                 (bases 1 to 503)
   AUTHOR (AU):
                              Marra, M.; Hillier, L.; Allen, M.; Bowles, M.; Dietrich, N.;
                              Dubuque,T.; Geisel,S.; Kucaba,T.; Lacy,M.; Le,M.;
                              Martin, J.; Morris, M.; Schellenberg, K.; Steptoe, M.; Tan, F.; Underwood, K.; Moore, B.; Theising, B.; Wylie, T.; Lennon, G.; Soares, B.; Wilson, R.; Waterston, R. The WashU-HHMI Mouse EST Project
   TITLE (TI):
   JOURNAL (SO):
                              Unpublished (1996)
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                        Location
                                                       Qualifier
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                                                   /lab-host="DH10B"
                                                   /note="Organ: embryo; Vector:
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                                                   MluI; Site-2: SalI; Cloned
                                                  cDNAs were cloned into the
                                                   MluI/SalI sites of a modified
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pBluescribe vector using

GLERCLEDHELVVQVESTMASESKFLFRKNYAKY

EFFKNPMNFFPEQMVTWCQQSNGS

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   481 ctgtgctagg atggctgttt agc
L2
     ANSWER 153 OF 156
                          GENBANK.RTM. COPYRIGHT 2004 on STN
LOCUS (LOC):
                        HSU69276
                                     GenBank (R)
GenBank ACC. NO. (GBN): U69276
GenBank VERSION (VER):
                        U69276.1 GI:1546834
CAS REGISTRY NO. (RN):
                        181109-72-8
SEQUENCE LENGTH (SQL):
                        2504
MOLECULE TYPE (CI):
                        mRNA; linear
DIVISION CODE (CI):
                        Primates
DATE (DATE):
                        17 Sep 1996
DEFINITION (DEF):
                        Human hGrbIRbeta/hGrb10 (GRBIRbeta/GRB10) mRNA.
                        complete cds.
                        human.
SOURCE:
ORGANISM (ORGN):
                        Homo sapiens
                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                        Hominidae; Hómo
639 a 652 c
NUCLEIC ACID COUNT (NA): 639 a
                                         654 q
                                                 555 t 4 others
REFERENCE:
                        1 (bases 1 to 2504)
   AUTHOR (AU):
                        Frantz, J.D.; Giorgetti-Peraldi, S.; Ottinger, E.A.;
                        Shoelson, S.E.
   TITLE (TI):
                        Human GrbIRbeta/Grb10: Splice Variants of an Insulin
                        and Growth Factor Receptor-Binding Protein with PH and
                        SH2 Domains
                        Unpublished
   JOURNAL (SO):
                        2 (bases 1 to 2504)
Frantz,J.D.; Giorgetti-Peraldi,S.; Ottinger,E.A.;
REFERENCE:
   AUTHOR (AU):
                        Shoelson, S.E.
   TITLE (TI):
                        Direct Submission
   JOURNAL (SO):
                        Submitted (04-SEP-1996) Research Division, Joslin
                        Diabetes Center, One Joslin Place, Boston, MA 02215,
                        USA
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                    Location
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CDS
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                288..1898
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                                        a potential SH3 domain interaction
                                        site; insulin receptor binding
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                                        and EGF receptors; splice variant of hGrbIR; member of the
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                                        /codon-start=1
                                        /product="hGrbIRbeta/hGrb10"
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                                        /db-xref="GI:1546835
                                        /translation="MNASLESLYSACSMQSDTVP
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                                        AIPNPFPELCGPGSPPVLTPGSLP
                                        PSQAAAKQDVKVFSEDGTSKVVEILADMTARDLC
                                        QLLVYKSHCVDDNSWTLVEHHPHL
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QTQLLQNFLNSSSCPEIQGFLHVKELGKKSWKKL YVCLRRSGLYCSTKGTSKEPRHLQ LLADLEDSNIFSLIAGRKQYNAPTDHGLCIKPNK VRNETKELRLLCAEDEQTRTCWMT AFRLLKYEMLLYQNYRIPQQRKALLSPFSTPVRS VSENSLVAMDFSGQTGRVIENPAE AQSAALEEGHAWRKRSTRMNILGSQSPLHPSTLS TVIHRTQHWFHGRFSREESHRIIK QQGLVDGLFLLRDSQSNPKAFVLTLCHHQKIKNF QILPCEDDGQTFFSLDDGNTKFSD LIQLVDFYQLNKGVLPCKLKHHCIRVAL"

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          61 ctgaccctgc tggagtctgt cccctgggct accctctgct tccccccatt gtgagtggtc
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L2
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Primates 6 May 1998

human.

Homo sapiens

Homo sapiens

Hominidae; Homo 631 a 652 c

(bases 1 to 2376)

Grb14

583 g

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;

510 t

Daly,R.J.; Sanderson,G.M.; Janes,P.W.; Sutherland,R.L.

Cloning and characterization of ***GRB14*** , a

mRNA, complete cds.

DIVISION CODE (CI):

ORGANISM (ORGN):

AUTHOR (AU):

TITLE (TI):

NUCLEIC ACID COUNT (NA): 631 a

DATE (DATE):
DEFINITION (DEF):

SOURCE:

REFERENCE:

novel member of the GRB7 gene family J. Biol. Chem., 271 (21), 12502-12510 (1996) JOURNAL (SO): OTHER SOURCE (OS): CA 125:27254

FEATURES (FEAT):

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2281 ttacaaaaa atagtttgtg cattgcaaat aagcaaagac ttggattgac tttacattca 2341 tcatttaaaa ttcattagtt aaaattaaac cttagg L2 ANSWER 155 OF 156 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2004) on STN 2004:13636 AGRICOLA ΑN DN IND43619263 ΤI Improved glucose homeostasis and enhanced insulin signalling in ***Grb14*** -deficient mice. Cooney, G.J.; Lyons, R.J.; Crew, A J.; Jensen, T.E.; Molero, J.C.; ΑU

Mitchell, C.J.; Biden, T.J.; Ormandy, C.J.; James, D.E.; Daly, R.J.

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- English LA
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- 1999:27349 CONFSCI ΑN
- 99-039843 DN
- ***Grb14*** ΤI Novel FGF signaling pathway u binds to FGF receptor 1
- ΑU
- CS
- Reilly, J.F.; Mickey, G.; Maher, P.A.
 Dep. Cell Biol., Scripps Res. Inst., La Jolla, CA 92037, USA
 American Society for Cell Biology, 9650 Rockville Pike, Bethesda, MD
 20814, USA; phone: (301) 530-7153; fax: (301) 530-7139; email: SO ascbinfo@ascb.org; URL: www.ascb.org/ascb/, Abstracts available. Price \$45. Paper No. 1365.
 - Meeting Info.: 984 0478: 38th American Society for Cell Biology Annual Meeting (9840478). San Francisco, CA (USA). 12-16 Dec 1998. ASCB, Bio-Rad, Genentech, Jeol USA, Johnson & Johnson, Leica, Leadership Alliance, Mark-Rambar Family Foundation.
- DT Conference
- FS **DCCP**
- English LA
- STN INTERNATIONAL LOGOFF AT 15:32:52 ON 09 JUL 2004